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Title:
Metric versus non-metric skeletal traits : Which is the more reliable indicator of genetic distance?

METRIC VERSUS NON-METRIC SKELETAL TRAITS:

WHICH IS THE MORE RELIABLE INDICATOR

OF GENETIC DISTANCE ?

With special reference to crania

from ancient Greece and Egypt.

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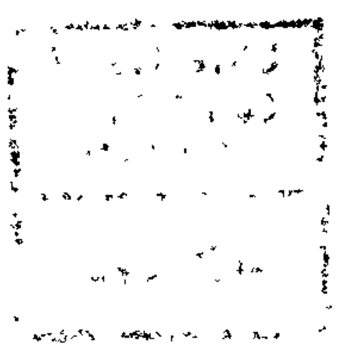
A thesis submitted to the University of Bristol

in accordance with the requirements for the degree of

Doctor of Philosophy in the Faculty of Science.

March 1989.



ABSTRACT

METRIC VERSUS NON-METRIC SKELETAL TRAITS: WHICH IS THE MORE RELIABLE INDICATOR OF GENETIC DISTANCE ?

With special reference to crania from ancient Greece and Egypt.

Judith E. Powell

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In studies of the affinity of human skeletal populations, morphological variation of the cranium is an important source of genetic information. Opinion is divided, however, as to whether the shape and size (metric variation) of the skull or its minor anatomical variants (non-metric traits) more closely reflect genetic distance. This work explores the controversy and attempts to resolve it by recording both types of trait in a series of ancient crania from Greece and Egypt. Taxonomic distances are then constructed and compared. The findings indicate that metric traits behave in a manner consistent with their having a strong genetic component. The pattern of group affinity produced by non-metric traits is less stable, varying according to sex, the number of traits used and whether the left or right side is considered. Even when sample sizes are small, metric variation is found to be the more valuable; methods of maximising the metric information obtainable from incomplete specimens are discussed. The genetic basis of non-metric variation, insofar as it can be represented by dichotomous scoring, is questioned. It is concluded that multivariate metric methods, which have lately been eclipsed by techniques employing non-metric data, are worthy of re-appraisal.

DEDICATION

This work is dedicated to my mother.

ACKNOWLEDGEMENTS.

First and foremost, I must express my gratitude to my joint supervisors for this thesis. Dr Jonathan Musgrave, who originally formulated the project and applied for funding, has given freely of his time and expertise. His knowledge of anatomy, archaeology and anthropology, as well as his great enthusiasm for the project, have been of inestimable value. Dr. Suzanne Evans I must especially thank for lifting the veil surrounding the mysteries of multivariate analysis, and for firing my enthusiasm for a subject I had previously found impenetrable. Thanks are also due to Professor Pickering for allowing me to undertake this work at the Department of Anatomy in the Medical School at Bristol University.

The funding for this work was provided by the Science and Engineering Research Council. I am grateful to the SERC for providing a three-year studentship and for reimbursing my traveling expenses for fieldwork in Greece.

In Greece, I received much help and hospitality from the following people: Mme. Vokotopoulou, director, and Mme. Despini, deputy director of the Archaeological Museum, Thessaloniki, who arranged access to the remains from Sindos and Pieria. They also generously provided me with accommodation at the museum for the duration of my stay in Thessaloniki. Special thanks are due to Despoina Ignatiadou who aided me on a day-to-day basis.

In Athens, I was greatly aided by associates of the American School at Athens. Dr Margo Camp of the Agora Museum kindly provided unlimited access to the Athenian remains which were stored there. Dr Martha Wiencke of the Argos Museum gave permission to study the crania from Lerna, stored at Corinth, while Dr Charles Williams arranged the practical side of this access.

I am extremely grateful to the staff and residents of the British School at Athens, for the pleasant and supportive environment offered by them. Dr Catling, the director, kindly gave permission to examine the remains from the osteotheke at Fortetsa, stored at the

British School's Hostel in Knossos, Crete. Dr Alan Peatfield, the curator at Knossos, arranged this access; Sheila Wall was also of help there as a fellow specialist in bones. At Knossos, I also examined the remains from Myrtos Pyrgos, for which permission I am grateful to Dr. Gerald Cadogan and Dr Jonathan Musgrave.

Back in England, my field work at the Duckworth Laboratory, Cambridge was kindly arranged by Dr J.P. Garlick of the Department of Physical Anthropology, who showed great interest in my project. I am also grateful to Dr George Mann, who demonstrated the different types of auditory torus, and discussed his own dissertation on that subject with me. Professor W.W. Howells must also be thanked for allowing the use of data that he had collected (the Teita and Giza).

Several miscellaneous folk must also be thanked for help given on various occasions. Dr. A. C. Berry helpfully provided details of the crania she had previously studied, for purposes of comparison. Shomarka Keita, who visited Bristol to present and discuss his own work in this field, also deserves many thanks. His emphasis of the importance of determining the genetic basis of the traits utilized was influential in this work. I am grateful to Professor C.D.Stephens of the Bristol Dental Hospital for demonstrating the use of the craniostat, and arousing my interest in dental anthropology.

I must mention here the staff of the Computer Centre at Bristol University, who have often given help with programming problems. Special thanks are due to Margaret Irish, who effectively became an unofficial supervisor in the last few months of my studentship, following Dr Evans's departure to Australia. I am also grateful to Dave Rogers for granting permission to use his program for plotting 3D graphs, and to Anne French for giving me advice on achieving a professional standard for my thesis using a word processor.

I would like to thank RoseMary Musgrave for her many kind words of advice and encouragement, and for her hospitality. Finally, Andrew Cheshire requires especial thanks for his patience and support, and also for acting as an unpaid computing consultant.

Author's Declaration

The work described in this thesis was the original and unaided work of the author. No part of this dissertation has been submitted for any other degree from the University of Bristol, or to any other university.

J. E. Powell.

(J. E. Powell)

1st March 1989

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1

INTRODUCTION.

1.1. Background to the study.

1.1.1. Anthropological contributions to archaeology.

Archaeologists have long been interested in tracing the movement of ancient peoples and have based their theories on evidence of similarities in the artifacts and cultural practices of roughly contemporaneous groups. They acknowledge, however, that the spread of a culture, as indicated by similar burial customs, types of pottery and architectural styles, is not necessarily accompanied by the movement of large numbers of people (Rouse 1985). It is here that they enlist the aid of anthropologists, in the hope that the biological characteristics of human remains will reveal affinity or dissimilarity between the groups in question. Rouse (1985), indeed, notes that in elucidating patterns of migrations in ancient times, "the best results have been achieved by a combination of archaeological, linguistic and physical anthropology research".

Anthropologists have documented a vast amount of variation in living peoples, reflecting differences in the gene pools of the groups. Morphological variants such as skin colour, physique, stature, dermatoglyphics and size and shape of the skull have been studied, as have biochemical variants such as blood group, enzyme and HLA antigen polymorphisms. Often with human remains from archaeological sites, skeletal morphology alone provides clues to the genetic affinity of the populations. This work is concerned with evaluating the extent to which morphological variants of the skull can be used to assess population affinity when dealing with archaeological remains.

1.1.2. The biological basis of human variation.

Variation in human populations arises since, although all members of the species have the same type and number of genetic loci, several different alleles may be present at a locus. It has been estimated that at least 30% of all gene loci vary (i.e. have two or more alleles)

within the human population (Bodmer and Cavalli-Sforza 1976, p.232). Any population may therefore be described in terms of the frequencies of certain alleles in the gene pool and this information can be used to derive a measure of *genetic distance* between groups. Where a large number of loci is studied, it may be assumed that the composite difference in the gene frequencies (strictly, the allele frequencies) between groups compares closely with the overall difference in the gene pools. These differences may reflect actual genetic relationships, such as the derivation of one group from another, or of two or more groups from a common ancestry, or the formation of a hybrid group from the mixing of two parental communities.

When living populations are studied, biochemical variants are of the greatest value, since actual gene frequencies can be derived. When morphological variation is considered the picture of genetic relationships becomes clouded. Morphological variation is generally continuous in nature, and the underlying genes almost entirely unknown. Each variant is considered to represent the additive effect of a large number of polymorphic loci, further modified by environmental influences, but major gene effects and pleiomorphism cannot be discounted. The extent to which morphological differences reflect gene pool differences is uncertain, but family studies and comparative assessments of morphological and genetic distances in living populations may provide clues. A review of these types of study will be found in chapter 2.

1.1.3. Morphological variation in the cranium.

For over a century now, morphological variation in the cranium has been the focus of studies of population affinity. It is generally accepted that skulls, jaws and teeth are the structures in which the effects of natural selection and the microevolutionary changes which follow can be most readily detected (Musgrave and Evans 1980). There is disagreement among craniologists, however, about which morphological features are the most reliable indicators of genetic distance. Some regard metric traits (cranial measurements reflecting size and shape of the skull) as the most rewarding sphere of study; others claim that minor morphological variants such as sutural bones, number and site of

foramina and bony bridges (collectively known as epigenetic, non-metric or quasi-continuous traits) are generally superior indicators of population affinity. The object of this work is to compare distance measures derived from both metric and non-metric traits, with a view to determining which type is the more useful for answering questions about population affinity.

1.2. Metric studies of population affinity.

1.2.1. The historical development of metric analyses.

Racial analyses based on the size and shape of the skull have a long history. The cephalic index (for living subjects) or cranial index (for dry skulls) was invented by Retzius in 1842 (Coon 1939) and still finds use today (Beals 1972, Beals, Smith and Dodd 1983). Indices represent one of the first attempts to define skull shape, though the assumption that indices are independent of size has been criticised by Blackith and Reyment (1971).

The use of measurement-based analytical methods necessitated the production of a precisely defined account of craniological technique. Broca in 1875 published a paper, 'Instructions craniologiques et craniométriques de la Societé d'Anthropologie de Paris' which fulfilled this need. In this work he defined exactly the points to be used in taking measurements, the measurements to be taken and the instruments to be employed. Prior to this, a number of more or less precise descriptions of cranial measurements existed, but these were for the most part tentative and unsystematic. Broca's craniological system received a wide acceptance and has formed the basis of many subsequent techniques (Penniman 1965).

The principal critic of methods of measurement and of the indices derived from them was Guiseppe Sergi. He contended that craniometry could be used to demonstrate anything one wished, and that many different racial forms could be obscured within the categories defined by indices such as the cephalic index. Sergi believed that drawings and photographs of the face, and cranial outlines (especially in norma verticalis) were of more value than measurements and indices. Cranial shape was therefore to be assessed by eye rather than by callipers. He devised a series of terms (ovoid, pentagonoid, beloid,

ellipsoid etc.) to describe the calvarial outline which could be used, along with criteria of facial shape, to distinguish races (Sergi 1894).

In a Europe obsessed with racial classification, Sergi's methods found favour. Many works appeared in which individual crania were allocated to set racial types or sub-races such as Nordics, Alpines, Mediterraneans and Dinarics (e.g. Myres 1930, Coon 1939, Charles 1965). These types were meant to reflect evolutionary trends in the descendents of Neanderthal and Cro-Magnon man. Angel (1971) classified the skulls from Lerna into six types or trends, with a number of sub-types within each. He noted, however, that these six reference points were abstractions of limited use since "no single modern population has ever been homogeneous enough to conform to any one such trend". Angel admitted that his system of types, based on "a number of growth tendencies" was "a stopgap until the time when twin and genealogical studies will reveal actual genetic components of skull growth".

A more fruitful approach has been the abandonment of the concept of racial types in favour of non-classificatory measures of distance between populations, where the *differences* between groups are of more interest than the classification of groups. The development of these methods owes much to the Belgian scientist Quetelet. Using large quantities of anthropometric data, he plotted frequency histograms and showed that the curves produced were similar to the 'Normal Curve of Error' described by Gauss. In the 'Physique Sociale', 1835, (greatly enlarged in 1869) and in the 'Anthropométrie' of 1871, Quetelet laid the foundation of all mathematical study of anthropological data (Penniman 1965). Following this introduction of the concept of central tendency, and the demonstration that biological variables tended in many cases to a standard form of distribution, the way was opened for studies based on the comparison of central tendencies by such workers as Galton and Pearson. This in turn suggested comparisons of the means with allowances made for the amount of variation which was present (Hursh 1976).

Many of the familiar basic statistical tests were instigated, developed or refined by Pearson around the turn of the century. The product moment correlation coefficient was one of these. Finding human crania to be particularly useful subjects to which to apply his methods, Pearson asked Flinders Petrie to send him the very large Egyptian E series -

nearly 1800 skulls - from Giza as material for measurement of correlation and variation. This was the stimulus for a long series of investigations into cranial form, spanning 30 years from 1900 onwards, at the Biometric Laboratory at University College, London (Howells 1969a).

The univariate methods employed by Pearson were, however, subject to serious limitations. These became plain when interest shifted from correlation and variation to population comparisons. Group relationships had to be inferred by a mental summing up of differences in the separate measurements and their significances, closeness of the mean values being taken to indicate propinquity. Pearson's Coefficient of Racial Likeness (Pearson 1926) was an attempt to quantify this problem and produce a single measure of distance from the amassed parameters.

This analysis of individual measurements failed to detect the difference in shape resulting from small absolute differences in opposite directions. To illustrate this with an example, the orbits of group A might, say, be marginally higher and less broad than those of group B, giving an overall appearance of comparative roundedness, but this difference in orbital shape would not be detected if the mean values for height and breadth in the two groups did not differ significantly. It was in response to the inability of univariate statistics to consider more than one variable at a time, that multivariate statistical methods were developed.

The vital concept underlying the use of multivariate methods is that the complete set of measurements taken from a single cranium represent a metric profile of that individual, called, in mathematical terms, a vector. If each of the measurements is simply used by itself to find the mean and variance of the measurement, this vector is dismembered and the individual lost (Howells 1969a). Bronowski and Long (1951) stressed that a bone should be regarded as a unit and not as a "haphazard jumble of piecemeal measurements". Any measurement should be judged in the context of all the other measurements in the same specimen. In the same way, the individual must be seen in the context of a population; these two requirements are achieved through the formation, from the individual vectors, of a

matrix of variation and covariation. This variance-covariance matrix (also called a dispersion matrix) is the mathematical basis for all multivariate analyses.

Multivariate methods were first proposed by Galton, who, around 1890, suggested that the observed correlation between measurements might be due to their joint correlation with unobservable but biologically significant causes. This idea was, however, not pursued by Pearson, who recognised that correlation would affect his Coefficient of Racial Likeness, but did not consider that this was worth compensating for exactly. It was not until the 1920s and 30s that multivariate statistical theory was developed, mainly by Fisher, though Mahalanobis, Hotelling and later, Rao also made important contributions (Howells 1969a). However, as the computations involved in multivariate analysis are cumbersome, these methods did not become widely used until modern high-speed computers and statistical packages to carry out the analyses became available. In recent years, multivariate methods have been utilized in several craniometric studies with satisfactory results (e.g. Mukherjee, Rao and Trevor 1955, Crichton 1966, Hiernaux 1966, Howells 1966a, 1970, 1973, Carlson 1976, Rightmire 1976, Van Gerven, Armelagos and Rohr 1977).

The most significant recent development in the history of population studies has been their incorporation within the discipline of numerical taxonomy. Since the 1930s some of the methods developed primarily with human cranial measurements have been used increasingly in taxonomic investigations of the variation of quantitative characters in many groups of animals and plants. The publication in 1963 of Sokal and Sneath's *Principles of Numerical Taxonomy* drew together and gave direction to research into phylogenetic relationships based on phenotypic characters.

Numerical taxonomy is the non-traditional school of taxonomy which derives a classification of units on the basis of numerical information about their affinities or differences, without recourse to information from inferred evolutionary history. This numerical information may reflect morphological phenotypes (phenetic taxonomy), protein structures or genes. Central to the method is the definition of a 'taxonomic distance' (though in anthropology the term 'genetic distance' is more commonly encountered) between the units studied. From these distances, phylogeneticists derive trees or dendrograms

(cluster analysis) which portray affinities between the units. Alternatively, ordination methods are used which portray the units as points in space, the distances between the points reflecting the taxonomic distances.

Numerical taxonomic methods have been extended to the study of groupings at the intraspecific level; it is to this category that human population studies belong. Sneath and Sokal (1973) advise caution, however, in the use of clustering methods in such studies:

> There is some doubt even about whether meaningful hierarchic structures can be obtained below a given categorical level. Whether this level is below that of the species . . . , or whether nonhierarchic phenetic relations begin at a higher level needs further investigation.

For this reason, ordination methods are employed for the portrayal of group affinities in the present work.

1.2.2. The choice of distance measure.

As noted earlier, the definition of a taxonomic distance between two groups, based on quantitative variates, is the first step in the analysis of racial affinity. Gower (1972) reviewed the different measures of distance which have been proposed, noting that they were of three main types; Czechanowski's DD (1932), Pearson's coefficient of racial likeness, CRL (1926) and Mahalanobis' distance, D^2 (1936). Writing $\bar{x}_{ij}$ to represent the mean of the *i*th of *v* variants in the *j*th population, where $\bar{x}_{ij}$ is measured in standardised units, the formulae are as follows:

1. Czechanowski's DD:

$$DD_{jk} = \frac{1}{v} \sum_{i=1}^{v} | \bar{x}_{ij} - \bar{x}_{ik} |$$

2. Pearson's coefficient of racial likeness:

$$CRL_{jk} = \frac{1}{v} \sum_{i=1}^{v} (\bar{x}_{ij} - \bar{x}_{ik})^2$$

3. Mahalanobis' Distance:

$$D^2_{jk} = (\bar{x}_j - \bar{x}_k)' W^{-1} (\bar{x}_j - \bar{x}_k)$$

For the Mahalanobis' distance, $\bar{x}_j$ is the column vector of means for the *j*th population, and W is the pooled within-population dispersion matrix (assuming that this pooling is

legitimate). Standardisation of the variables is unnecessary as one of the effects of multiplying by W^{-1} is to eliminate the effects of scale change.

The relationship between these three coefficients was discussed empirically by Huizinga (1962) who found little difference between them and hence suggested that the simplest measure, DD, should be used. His method of comparing the three coefficients was, however, criticised by Gower (1972), who maintained that each of these statistics had distinct characteristics.

As Gower points out, the choice of distance statistic depends on what is required of it. CRL and D^2 are actually squared distances and if large differences in a few variables are considered to be taxonomically more important than small differences in many variables, then a squared difference is to be preferred, though with D^2 and CRL it is the square root which gives the Euclidian distance. It could be argued that measurement error, always a problem in anthropometrics, will have a smaller distorting effect if squared distances are employed; small differences between group means may be entirely due to measurement error, but large differences, which contribute proportionately more to the final distance, should be less affected.

D^2 differs fundamentally from the other distance measures since it takes account of intercorrelations of the traits and discards redundant information. CRL was often criticised for not taking account of correlations, though Gower argues that in some cases CRL may be a more appropriate measure than D^2. He believes that the human mind distinguishes between groups *because* there are correlated characters within the groups, and that of the three statistics, DD and CRL alone quantify this idea. Where populations have already been established, however, D^2 is the most useful statistic.

The archaeological groups utilized in this work are separated both geographically and chronologically, and it seems appropriate to regard them as separate populations. Mahalanobis' D^2 is therefore the statistic of choice, and is the one utilised here. Like CRL, but unlike DD, it has a Euclidian representation, which is useful since the groups can be plotted. D^2 does not, however, take into account missing data values, or different sample sizes. Rao (1952) has given a formula for correcting the bias in D^2 caused by different

sample sizes, though if the two groups are closely related, this correction may produce a negative squared distance value. Rao's correction is further discussed in section 3.2.2.1.

1.2.3. Some criticisms of the multivariate approach.

The undoubted elegance of the theory of multivariate analysis has led to the utilisation of these techniques for investigating a wide variety of morphometric problems. In recent years, the exponential growth in the number of such studies has evoked some scepticism about the value of these methods (e.g. Kowalski 1972, Szalay 1974, Lewis 1977). These critics view the ready availability of computer packages as a mixed blessing; though they are undoubtedly time-saving, they do allow workers with an incomplete appreciation of statistics to undertake and interpret complex analyses without considering if their interpretation is valid. Thomas (1976) comments:

> Computers are seductive devices which tend to lure the unwary down the endless trail toward numerical obscurity . . . what good is an orthogonal multiple-factor multivariate analysis if one doesn't understand the meaning of elementary correlation?

Nevertheless, these critics acknowledge the potential strengths of the morphometric approach; many of their criticisms are directed against abuses of these methods rather than the methods themselves. Corruccini (1978) gives an instructive and cautionary account of the many ways in which multivariate methods may be misused.

It should be remembered that the rationale for using a statistic is the *simplification of the original data,* usually by reducing their dimensionality. Kowalski (1972) makes a pertinent point:

> While this approach may in fact occasionally produce the required simplification, it is more usually the case that the new dimensions defy meaningful interpretation and that no real simplification is realised. . . .

Kowalski believes that multivariate methods are frequently too complex to use and difficult to interpret; consequently he believes univariate methods to be of more value. Corruccini (1978) counters that univariate output may similarly be used to obfuscate the reader by presenting an overwhelming array of tables. Nonetheless, Kowalski's advice on the criteria for employing multivariate methods is sound:

> When we have sufficient data, when the assumptions underlying the use of the technique are justified, when we can interpret and communicate the results of the analysis and when multivariate methods contribute insight over and above that which can be achieved using simpler methods their use is certainly justified. When these criteria are not satisfied it would appear that some case could be made for the employment of simpler procedures.

Bearing this criticism in mind, a univariate analysis of the groups employed in this study is undertaken as a preliminary and accessory consideration to the multivariate analysis.

For clarity of thought, it is important to distinguish between the purely mathematical output of the techniques, and the biological interpretation placed upon these results. Statistical computer packages process numbers irrespective of what they are meant to represent and, always provided that the distributional assumptions implicit in the techniques are observed, the numerical output can be viewed with complete confidence. The biological interpretation of results is, however, a minefield in which the experimenter must tread most carefully. Again, Kowalski's comments on multivariate methods are appropriate:

> No one really questions the mathematics on which they are based. . . . (but) mathematical artifacts may not be interpretable in the context of the subject-matter problem . . .

Yet, without interpretation of the results there may be very little point in carrying out an analysis at all! The interpretation of genetic distances is discussed in section 1.5, but some general points will be made here.

A motto used by computer programmers is instructive in this situation, viz. "garbage in - garbage out"! If the numbers extracted from an analysis are to be viewed in a certain light, the numbers fed into it must be similarly appraised. Corruccini (1978) complains that too many functional morphometric studies have been carried out using measurements which, in themselves, have little functional meaning. In the present study, the distances extracted are to be interpreted as genetic distances; consequently, the variation in the measurements used should ideally reflect only genetic factors. Since this is impossible when using measurements, steps should be taken to minimise error by utilising only those measurements which are believed to have a high genetic component to their variation. In chapter 2 the evidence for the genetic basis of measurements is reviewed.

An alternative interpretation of multivariate distances discards genetic considerations and regards the distance as indicative of size and shape differences in the sample - a phenetic distance rather than a genetic distance. This interpretation is commonly used by numerical taxonomists when studying aspects of form. It is particularly appropriate when considering different species, since very little is known of the genetic mechanisms responsible for major differences in form (Hitching 1983). This interpretation, however, leads to another consideration; the vexing problem of size and shape.

Multivariate methods have been criticised on the grounds that they separate units on the basis of size rather than shape (Bookstein 1978, Corruccini 1987, 1973). Where the aim of the study is to elucidate taxonomic or functional relationships between different species, then shape difference, rather than size difference should be the prime consideration. With methods such as canonical variate and discriminant function analysis, the extent to which the results are driven by size rather than shape seems to depend on the relationship between the within-group and between-group variance (Albrecht 1976). Various techniques have been suggested for separating size and shape factors (reviewed by Corruccini 1987, 1978), but controversy remains regarding the appropriateness and effectiveness of these methods.

Corruccini (1978) notes that multivariate analyses based on unmodified measurements work well only when general size variation falls within a restricted range, when a size difference automatically causes a shape difference. When dealing with individuals at the subspecific level, however, size and shape may be inseparable components of form. Consequently, the consideration of size and shape components is felt to be unnecessary in this work.

Other practical difficulties arise when utilizing archaeological populations which make the data 'messy' and consequently have a bearing on the interpretation of the output. Since man is a sexually dimorphic species, the sexes must be examined separately, and the sexing of remains on biological criteria alone is often unreliable. Grave artifacts may give clues to the sex of the occupant, but in practice the interpretation of such artifacts may not be straightforward. Age is also known to have an effect on cranial dimensions (Israel 1973,

1977), even in adults, so that the groups to be compared should ideally have a similar distributions of age groups. Current methods for the determination of skeletal age are, like sexing, somewhat unreliable. (Brothwell 1981).

The condition of the crania also affects the quality of the analysis; damaged or fragmented skulls may defy accurate measurement, while cranial deformation (cultural or due to earth pressure) may render individuals of little use to the study, thus reducing sample sizes and introducing more uncertainty. Even when the samples are large and in good condition, measurement error cannot be avoided. These points will be further explored in section 3.2.2.2, where suggestions for minimising error will be made.

1.3. Non-metric studies of population affinity.

1.3.1. The historical development of non-metric analyses.

Minor variations in cranial morphology, such as sutural ossicles, ridges, bridges and foraminal anomalies, have aroused the curiosity of anatomists for over a century. Chambellan (1883, cited by Dorsey 1897), in an anatomical and anthropological study of wormian bones, first suggested the possibility of using such traits as anthropological characters. Dixon (1900) discussed the channels on the external surface of the frontal bone, corresponding to the branches of the supraorbital nerve, in various races. Their occurrence, he found, varied from hardly any in Australian aborigines to over 50% in Negro populations. Russel (1900) first presented a study where data on the incidence of several variants in American populations was gathered together, though he was unable to draw any overall conclusions regarding group affinity.

The interest exhibited in these traits led to the publication by Le Double (1903, 1906) of an encyclopaedic survey of these anomalies in the human skull and vertebral column. Wood-Jones (1931a, 1933) also believed that such traits could be used as a criterion for racial diagnosis, though his evaluation of the data was entirely subjective.

It was Laughlin and Jørgensen (1956) who first utilised a number of these traits in a statistical distance analysis to demonstrate genetic separation between Greenlandic Eskimo crania. They studied 8 cranial variants in 4 breeding isolates of Eskimo and, using a variant

of Penrose's (1954) size and shape statistic to analyse the data, suggested the probable historic relationship between these populations. Following this work, 10 such characters from 14 widespread populations were employed by Brothwell (1959) to ascertain their value in differentiating larger groups of mankind. Brothwell (1959) also constructed 'isoincidence' lines from some of the variants, in the same way that blood group frequency maps have been drawn.

This utilisation of non-metric traits as population indicators rested on the assumption that this variation has a genetic, rather than environmental basis. Evidence for the genetic nature of these traits in man came from a number of family studies (e.g. Montagu 1937, Torgersen 1951a, b, Selby, Garn and Kanareff 1955, Suzuki and Sakai 1960) where one particular type of trait was investigated. These studies generally concluded that the traits were inherited, usually 'by a dominant gene with incomplete penetrance'. The observation (Brothwell 1959) that the frequency of any particular variant was constant in a given race, and similar in related races was also suggestive of a genetic basis. However, the major breakthrough in elucidating the mechanisms controlling trait expression occurred in the 1950s. This came from a series of investigations by Grüneberg and his co-workers, at University College, London, into the inheritance of skeletal traits in the mouse (summarised in Grüneberg, 1963).

Grüneberg discovered that a range of minor variants in the skeletons of inbred strains of laboratory mice , although manifesting as "all or none" characters, were inherited as continuous variables rather than as Mendelian traits. These traits exhibit a wide range of morphological expression but they are all distinguished by having a discontinuous distribution based on an inherited underlying continuous variable - Grüneberg (1952) coined the term 'quasi-continuous' for this type of discontinuous variation.

Grüneberg (1963) demonstrated that the actual inherited entity is the size or rate of formation of an embryonic rudiment and not the presence or absence of a variant in the mature skeleton. In the CBA strain of mice, for example, 18% of adults lack one or both of their lower third molars. There are apparently genes which control tooth size as such, shown by the increased variance of third molar size in the hybrid offspring of two inbred

strains. Strains of mice in which the incidence of missing molars was high also had on average, smaller molars than other strains. Grüneberg showed that in embryonic mice, there was a range in size of the tooth germ at any particular stage, but that if the tooth germ failed to reach a certain size by the sixth day after birth, the tooth germ regressed and the tooth failed to develop.

Grüneberg also found that the factors determining whether a tooth will develop or not are the environmental factors connected with maternal physiology. For example, tooth loss was commonest in large litters and in first litters where the size of the young was small at birth. Third molar size could be increased by fostering the young onto mothers whose lactational performance was better than that of the natural mother, or decreased by feeding the mother on a deficient diet which interfered with lactation.

For any inbred strain, the frequency of a trait was found to be constant in each generation, and that the trait frequency was a characteristic of the gene pool in question. Moreover this frequency was found to be largely independent of age, and usually sex, so that it could be used as a genetical marker in population studies in approximately the same way as the frequency of a blood group. Furthermore, there are in the mouse very few correlations of the joint occurrence of pairs of variants.

Grüneberg's work influenced R. J. Berry, who utilized non-metric traits in studies of wild populations of house and fieldmice (1963, 1964, 1965). He compared island populations with those from the mainland and concluded that non-metric traits were valuable indicators of the population gene pool. Later, with A. C. Berry, he used these traits to study human populations, introducing the term 'epigenetic' to describe the variants. Berry and Berry published their paper "Epigenetic variation in the human cranium" in 1967 and this promoted a surge of interest in the subject.

In this work they drew attention to the findings of Grüneberg and described in detail 30 non-metric cranial variants which provided a reference set used by many later workers. They also introduced to anthropologists the Grewal-Smith Mean Measure of Divergence (MMD), a statistic whereby the frequencies of several uncorrelated traits can be combined to form a single measure of divergence between groups. This measure, originally suggested by

C. A. B. Smith, had previously been used with success in studies of inbred mouse strains by Deol et al.(1957), Grewal (1962) and Searle (1964). Berry and Berry used the MMD to study the affinities of ancient Egyptians and Palestinians, and of some more widely separated groups.

Berry and Berry (1967) also argued that non-metric traits have many practical and theoretical advantages over metric traits, since they are unaffected by environment, very quick and easy to score and can be used on fragmented and deformed crania. They claimed that the lack of inter-character correlations make the computation of multivariate statistics much simpler than is the case for metric traits. Following this publication, many anthropological studies appeared which utilized non-metric traits (e.g. Berry, Berry and Ucko 1967, Kellock and Parsons 1970a, 1970b, Berry 1974, 1975, Finnegan and Marcsik 1979, Berry and Berry 1972, Kaul et al. 1979).

R. J. Berry (1968) has emphasised that it is the *probability* of exhibiting a character which is an inherited character, and hence the incidence in a population that is a genetic characteristic, and not its segregation in the individual. Nevertheless, methods have been devised which employ these traits to allocate an individual to a family group (Sjøvold 1976). Others have developed methods of racial classification (Finnegan and McGuire 1979, Cooprider, Rubison and Finnegan 1980, Finnegan and Rubison 1984) analogous to the discriminant function analyses used with metric traits (Giles and Elliot 1963, 1962) to allocate an individual to a particular sex or race. Finnegan and McGuire (1979) state that non-metric traits are exceedingly useful in classifying one skeleton into one of two populations, which groups need not represent major racial divisions. They also found the accuracy of classification to be as great as, or greater than, that of discriminant statistics based on traditional metric variation.

1.3.2. The choice of distance measure.

Three main categories of statistic have been employed to create a taxonomic distance based on non-metric trait. These are:

1. Variants of Penrose's (1954) size and shape statistic, used by Laughlin and Jørgensen (1956) and Brothwell (1959).
2. Variants of the Grewal-Smith Mean Measure of Divergence (MMD) as used by Berry and Berry (1967) among others. Several improvements to the original MMD formula have been suggested by Sjøvold (1973) and Green and Suchey (1976)
3. Genetic distance formulae, designed originally for situations of multiple alleles at a single locus, but perhaps suitable for non-metrics (Malyutov et al. 1972). Zegura (1975) employed such a distance, viz. Balakrishnan and Sanghvi's (1968) B^2, in his study of Eskimo crania.

Examples of the three types of formula are given below, where:

θ_{ij} and ϕ_{ij} are the transformation angles of the *i*th trait in the *j*th sample,
$n^{ij}_{..}$ is the size of the sample *j* for the *i*th trait,
$p^{ij}_{..}$ is the trait frequency ,
k is the count of positive observations for the trait,
R is the total number of traits used:
M is the total number of populations

1. Laughlin and Jørgensen's (1963) coefficient of divergence (CD).
(A variant of Penrose's (1954) size and shape statistic.)

$$CD = \sqrt{\sum_{i=1}^{R} \{ (\phi_{ij} - \phi_{ik})^2 / R \}}$$

where ø is an angular transformation of the form

$$\phi = \text{asin} \sqrt{\frac{k}{n+1} + \frac{k+1}{n+1}}$$

2. Grewal-Smith Mean Measure of Divergence (MMD), used by Berry & Berry (1967)

$$MMD_{jk} = \frac{1}{R} \{ \sum_{i=1}^{R} [(\theta_{ij} - \theta_{ik})^2 - (1/n_{ij} + 1/n_{ik})] \}$$

where θ is an angular transformation of p, the trait frequency, of the form

$$\theta = \text{asin} (1 - 2p).$$

3. Balakrishnan and Sanghvi's (1968) B^2. (Zegura 1975)
(adapted for dichotomous traits.)

$$B^2_{jk} = \sum_{i=1}^{R} \{ (p_{ij} - p_{ik})^2 / C_i \},$$

where C_i is the common variance of trait *i* over all M populations, such that

$$C_i = \sum_{m=1}^{M} \{n_{mi} p_{mi} (1 - p_{mi})\} \; / \; \sum_{m=1}^{M} n_{mi}$$

As with the metric distances discussed in 1.2.2, these three measures have differing properties. The value of CR lies between 0 (identity) and 180 (maximum dissimilarity). The MMD can have negative as well as positive values, with a theoretical range from approximately -1 to +10. Both CD and MMD use an angular transformation to render the sample variance of the trait frequency independent of the value of p. The MMD, however, also contains a term ($1/n_{ij} + 1/n_{ik}$), to allow for sampling fluctuations. B^2 is a complex statistic originally designed for multi-state characters, which is much simplified for dichotomous traits. It ranges from 0 to infinity and it gives more weight to characters with frequencies near 0 and 1; its square-root, the distance B, is the only Euclidian distance amongst these three. All three types of formula assume that the individual traits are uncorrelated.

The most frequently used statistic has been the MMD, or some variation on that formula. Berry and Berry (1971) state that the MMD has the advantage that the computations involved are extremely simple, and that the statistic is related to the Chi-square distribution, from which the significance of the distance obtained can be found. Moreover, they claim that the answers obtained by the MMD and Penrose method are similar.

Most variants of the Grewal-Smith formula involve different angular transformations. Green and Suchey (1976) present evidence that the Smith-Grewal angular transformation does not adequately stabilize the variance where sample sizes are small, especially when p is also small. They suggest alternative transformations, and give the necessary adjustments to the MMD formula, which do a much better job of stabilizing the variance. One of these alternatives, the Freeman-Tukey transformation, is adopted in the current work (see chapter 3 for the formula). Finnegan and Cooprider (1978), however, compared 13 different formulae for distance measures on a single data set, and found good

agreement between all of them. They therefore recommended that, where sample sizes are adequate, there is no reason for abandoning the simpler Grewal-Smith MMD.

Berry and Berry (1971) record a suggestion by C.A.B. Smith that the MMD statistic is improved by taking the square root of the MMD. This ensures that, to a first approximation, the distance is Euclidian. The raw MMD is non-Euclidian, which often makes interpretation of tables of distances difficult. Notwithstanding, the use of the square root has not been pursued by other authors, perhaps because negative MMDs are so frequently encountered.

1.3.3. Criticisms of the non-metric approach.

Following the increased popularity of non-metric studies, critical appraisals of the method began to appear. Ossenberg (1970) warned that artificial deformation of the cranium could affect the incidence of some traits, most notably the sutural ossicles, and showed that some traits were subject to age effects even in adulthood. Corruccini (1974) questioned whether the assumptions of lack of sex associations, and lack of intercorrelations were justified, though A. C. Berry later found no evidence (1975) of significant age or sex effects or inter-trait correlations. Perizonius (1979a) drew attention to the problems caused by asymmetrical expression of bilateral traits when calculating trait frequency.

Sjøvold (1973) discussed some of the problems raised by the occurrence of different numbers of observations (sample size) for each individual trait within a group. She demonstrated that those traits with fewer observations (e.g. midline traits as compared with bilateral ones) contributed less to the final measure of divergence. Similarly, when incomplete crania are examined (a situation in which the superiority of non-metric over metric methods is contended) this weighting may mean that the MMDs are not strictly comparable if traits common in one group are rarely observed in another. Sjøvold also recommended that traits whose variance, compared with the sum of the other variances, is very large be omitted, since this usually indicates that there are too few observations.

One noticeable feature of non-metric studies is the frequent occurrence of anomalous distance values in otherwise successful studies. Berry and Berry (1967) found a surprising

lack of distinctiveness between West Africans and North Indians, and a greater similarity between Egyptians and West Africans than between Egyptians and Iron Age Palestinians. In a later study (1972), the medieval Scots appeared more closely related to ancient Egyptians than were the Palestinians. Conversely, skeletons from the late Egypto-Greek cemetery at Hawara were not well distinguished from earlier 'pure' Egyptian series. Musgrave and Evans (1980) maintain that these anomalies prove non-metric traits to be unreliable indicators of population affinity. An alternative interpretation is given by Brothwell (1981), who comments that non-metric traits are more suited to the study of closely related groups than distant ones. This conclusion is also shared by Corruccini (1974, Kaul, Anand and Corruccini 1979).

1.4. The aims of this study.

For many years now, workers investigating the degree of affinity between groups of ancient human populations have employed metric and non-metric skeletal traits. Both the former (continuous) and the latter (discontinuous) type of variation have been claimed to reflect reliably differences in the gene pools of the groups under study. There is still no consensus, however, as to which, if any, type of trait is superior. Ossenberg (1970, 1976, 1977), Gaherty (1974) and R. J. and A. C. Berry (1967, 1972, 1974, 1979) have argued vigorously in favour of non-metric variation. Rightmire (1972) conversely, could not confirm with discrete traits the results (consistent with other data) which he obtained from metric variables. Carpenter (1976) also concluded that non-metric traits have little discriminatory value in racial studies.

Some authors have suggested that both types of trait be used in a complementary fashion. Corruccini (1974, 1976) notes that the information carried in each is seemingly not redundant; Cheverud, Buikstra and Twichell (1979) consider that one category cannot justifiably be preferred over the other. Furthermore, both workers present evidence that non-metric traits are not independent of the general size and shape of the craniofacial complex.

The primary objective of this study is to determine which type of morphological trait, metric or non-metric, is the more reliable indicator of genetic distance. The materials employed are cranial samples derived mainly from Greek and Egyptian archaeological sites. From each of these samples, metric and non-metric traits are recorded and used to construct taxonomic-distance measures between the groups.

When ancient crania, rather than living peoples, are the subject of study, data on gene frequencies for that population are not generally available. The question as to which morphological distance most closely resembles the genetic distance cannot therefore be answered by direct comparison. An oblique approach to the problem must therefore be taken, namely, that the properties and behaviour of the morphological distances must be examined, to see which type corresponds most closely with the properties of a genetic distance. Following the example of Zegura (1975), this is achieved by examining the sexes separately. In the absence of any unusual mating patterns (such as exogamy), genetic distances derived from males and females would be expected to be almost identical. The extent to which morphological distances derived from both sexes concur may therefore be regarded as a measure of the reliability of the morphological distance as an indicator of genetic distance.

A further property of genetic distances relates to the hypothesis of non-specificity (Sokal and Sneath 1963). This theory states that there are no distinct large classes of genes affecting exclusively one class of characters or one anatomical region. If the non-specificity hypothesis holds, the implication is that similar patterns of affinity should result from different kinds of character or from different parts of the body. Moreover, genetic distances should reflect only the degree of difference in the gene pools; the actual genes chosen should not affect the pattern of population relationships. In the present study, this property of genetic distances is tested by comparing metric and non-metric distances, as well as those derived from different numbers of traits.

Subsidiary objectives of the study are a consideration of sources of error in the morphological distances, especially those occurring when these methods of analysis are applied to archaeological data. Procedures for reducing error will be discussed, and

suggestions made for overcoming the problems of small sample sizes and badly preserved material. Finally, the distances obtained from a set of 13 archaeological sites will be evaluated, to see if these distances give any useful information about patterns of migrations in ancient times.

1.5. A few comments on the term 'genetic distance'.

This term is often employed by anthropologists in studies of racial propinquity but its fuller implications are rarely considered. When used by taxonomists who hope to unravel the skeins of evolution by the study of protein and DNA variants in extant species, the distance is related to the length of time since the species emerged from a common ancestor, and it may be used to construct evolutionary trees whose branch points can be interpreted chronologically. In this case the differences between groups are due to genetic mutations, which must be assumed to occur at a constant rate if these studies are to have any value.

Genetic mutations are of limited use in the study of such a recently emerged species as man; allele frequencies (commonly called 'gene' frequencies), however, provide a considerable source of variation. Bodmer and Cavalli-Sforza (1976) defined genetic distance, for a single locus, as the square of the difference in the gene frequencies of two groups. The study of variation at a single locus is mathematically simple but as the number of loci considered rises, so does the difficulty of comprehending such variation. Some composite measure based on all the characteristics under consideration is therefore necessary, and several methods have been suggested (Nei 1972, Edwards and Cavalli-Sforza 1972, Balakrishnan and Sanghvi 1968). If such distances are to be interpreted from a chronological viewpoint (which is usually desirable) then the factors which cause gene frequencies to diverge must be identified, and the rate at which they diverge appreciated. If gene frequencies do not diverge at a constant rate, this must be compensated for in the construction of the genetic distance.

The well-known Hardy-Weinberg principle states that under conditions of random mating, with no selection, immigration or emigration, the frequency of any allele in a large population remains constant in each generation. In practice, departures from the Hardy-

Weinburg equilibrium, caused by random events in gametogenesis and fertilization, occur over a period of time, more markedly in small populations. This effect is known as random genetic drift. Cavalli-Sforza and Edwards (1967) argued that in order to reconstruct genealogical pathways from population gene frequency data, it is essential to adopt a specific model for the process of evolutionary divergence in gene frequency. They concluded that for fairly closely related groups, such as the races in man, changes in gene frequency are brought about by genetic drift, or by processes that closely resemble genetic drift.

Drift does not cause gene frequencies to diverge at a constant rate; they may rise or fall at random with each generation. Edwards and Cavalli-Sforza (1972), developing a method first proposed by Bhattacharyya (1946, cited by Edwards and Cavalli-Sforza 1972), introduced the concept of 'stochastic distance' modelled on the process of random fluctuations which occur in Brownian motion. With this model, any distance can be interpreted in terms of the probability of that distance being travelled in a certain time. Stochastic distances, which occupy curved space, are translated into Euclidean space (at the cost of over-estimating larger distances) in order to produce meaningful distances which can be used to construct evolutionary trees. Malyutov, Passekov and Rychkov (1972) derived a statistic for constructing genealogical trees based on stochastic processes which also allowed gene frequencies at the branching points to be estimated. They applied this method to ethnic isolates from the Russian-Mongolian border region and found that the time coordinates of the branching points agreed strongly with linguistic, historical and archaeological evidence.

Even such methods which take account of the random nature of gene frequency fluctuation are open to criticism. The effects of gene flow (migration) cannot be discounted in populations that live in close proximity, and if widely separated groups are utilized (Cavalli-Sforza and Edwards 1967, comparing Eskimo, Korean, Bantu and English), they are separated by such vast distances in time that many alleles may have undergone complete fixation, in which case genetic drift cannot be approximated by Brownian motion (Malyutov, Passekov and Rychkov 1972). The effective population size, which is important for the estimation of times of isolation, is also impossible to assess accurately;

allele frequencies may be drastically altered in one generation following a natural disaster which decimates the population. Finally, it is possible that the alleles utilized may be subject to natural selection, in which case gene frequencies are determined predominantly by the environment. It is difficult to rule out selection effects on individual alleles; even the ABO blood groups, used in numerous studies (e.g. Sanghvi 1953, Constandse-Westerman 1972) have been shown to have some selective value. Vogel (1970) showed that stomach cancer and duodenal ulcer occur with higher incidence in people of groups A and O respectively, so that selection may be acting on even these 'neutral' alleles. It is clear, therefore, that the interpretation of genetic distances from a historical perspective must be undertaken with caution.

In the study of ancient populations, where skeletons alone remain, it is almost impossible to determine gene frequencies directly. Some workers have attempted to derive gene frequencies from ABO blood groups (Lengyel 1984, Borgognini and Paoli 1969, Smith 1960), but the estimates are subject to errors from the action of bacteria and soil on the antigens (Brothwell 1981). The serological study of mummified tissue has met with more success (Hansen and Gürtler 1983, Strastny 1974) but for many archaeological populations, skeletal morphology remains the only criterion from which affinities may be judged. The question yet remains, can taxonomic distances derived from cranial morphology be interpreted in the same manner as genetic distances derived from blood polymophisms?

Skeletal traits, both continuous and discrete, are *polygenic*, that is, determined by the joint action of multiple genes, each having an equal and additive effect, and nongenetic influences. The effects of genetic drift and gene flow on such polygenic quantitative traits are not generally agreed on. Since drift and gene flow are the primary determinants of gene frequency differences among populations in a local area, the assessment of these forces on polygenic traits is crucial if the above question is to be answered.

Some (e.g. Howells 1973, Morton and Lalouel 1973) have argued that single locus and polygenic traits respond to drift and gene flow in essentially the same way. Others state that the two types of trait are affected differently. Drift is often seen as having little effect on polygenic traits, as random fluctuations tend to cancel one-another out if the

number of loci is large (Spielman 1973, Rothhammer et al. 1977, Froehlich and Giles 1981). This position is supported by Livingstone's (1972) computer simulation of drift in polygenic traits. It has also been suggested that polygenic traits tend to respond more slowly to gene flow than single locus traits, and this may be advantageous when studying long-term migration patterns (Hanna 1962). The two distances used in this work, the Mahalanobis D^2 and the MMD are not derived using stochastic principles, and are appropriate where gene flow, rather than drift, is seen as the major driving force for morphological change.

The title of this study implies that, in seeking to relate morphology to genetic distances, the genetic distance is the only index from which group relationships can be reliably established. This is the opinion of Cavalli-Sforza (1974), who asserts that single locus genes are much better indicators of change and distance than metric traits, the latter having been "changed by natural selection to fit the environment to a far greater extent than the rest of our genes have". Some workers, however, assert that morphological distances have advantages over single locus genetic distances. Hiernaux (1966), who examined anthropometric and genetic data from Central African tribes, considers that the metric data are the more valuable of the two:

> It is now suspected that the systems of red-cell and serum characters . . . react more to different environmental selective stresses than do the multifactorial, partly genetical morphological features, . . . In a problem requiring an assessment of the total difference between gene pools, . . . we should not drop anthropometric characters despite the fact that they cannot now be expressed in terms of gene frequencies and that they have an environmental component.

Dow and Cheverud (1985) concur with this view:

> anthropometric measurements show a significantly better fit to population processes, as represented by geography in the Yanomamo and migration distance at Bougainville, than single locus markers, and thus may be the preferred metric in microevolutionary reconstructions. The superior performance of anthropometric measurements may be due to the averaging of effects from a larger number of segregating loci and the possibility that antigenic, serum, and red cell protein genes may be a biased sample with respect to evolutionary processes.

Finally, the way in which the results are presented requires some consideration. In taxonomic studies, genetic distances are often depicted as a dendrogram or tree linking the species studied. This type of presentation has also been used for human populations, both for genetic (e.g. Cavalli-Sforza 1974, Malyutov, Passekov and Rychkov 1972) and

morphological distances (Guglielmino-Matessi et al. 1979, Zegura 1975). Only where random drift can be assumed to be the only factor of differentiation, is such clustering justified. Hiernaux (1972) advises against the use of dendrograms since "most living populations . . . result from multiple hybridisation processes" and the recent evolutionary history of man with its manifold gene exchanges and its tendency to converge does not conform to this assumption.

> In anthropobiology, it looks probable that only special cases strictly limited in space and time, conform closely enough to this model to permit the interpretation of dendrograms as evolutionary trees. (Hiernaux 1972)

For this reason, among others, the present work does not use cluster analysis to derive dendrograms, but uses ordination methods to represent distances graphically. Hence, patterns of similarity may emerge which can be interpreted in the light of geographical, chronological and archaeological considerations.

2

GENETIC FACTORS IN CRANIAL MORPHOLOGY.

Since the taxonomic distances derived from morphological traits are to be regarded as genetic distances, this necessitates an investigation of the extent to which morphological variation reflects the underlying genetic variation. Evidence in the literature pertaining to this question will now be discussed.

There are several methods of investigating this question. The three types of study reviewed in this section are:

1) Ones which arrive at an estimate of the *heritability* from a consideration of the trait variance in relatives.
2) Ones which examine traits in hybrid populations and compare them to the parent groups.
3) Ones which derive taxonomic distances from morphological traits, then compare them to genetic distances derived from serological and blood group gene frequencies, or to non-biological distances constructed from linguistic data, archaeological inferences and geographic distance.

Finally, evidence for the way in which non-genetic factors can influence cranial morphology will be briefly considered.

2.1. Heritability studies: some general considerations.

Heritability is defined as that portion of the variance which is due to additive genetic effects. It is the additive genetic component, otherwise known as the 'breeding value', which determines the degree to which offspring resemble their parents. The remaining portion of the variance, the 'environmental' component also contains the non-additive genetic components (dominance and pleiotropic effects, as well as gene-environment interactions). This is heritability in the narrow sense; broad heritability or 'degree of genetic determination' is defined as the portion of the variance due to all genetic effects, as

opposed to deviations caused only by the environment. This is the heritability estimate which is derived from twin studies; parent-offspring and sib-sib studies produce estimates of the narrow heritability. The additive genetic component of the variance is not directly measurable, but the regression or correlation coefficients of the two types of relative are used, the heritability being the observed value as a proportion of the value that would be found if the character were completely inherited.

The concept of heritability itself is subject to serious limitations. Falconer (1981) points out that :

> heritability is a property not only of a character but also of the population and of the environmental circumstance to which the individuals are subjected.

The genetic components of heritability are influenced by gene frequency and would therefore be expected to differ between populations. Groups subject to widely varying environmental conditions would have lower heritabilities than ones developing under more uniform conditions. Hence, estimates derived from one population cannot with confidence be applied to another.

Heritability estimates are also subject to high standard errors, though those derived from parent-offspring relationships (especially mid-parent-mean-offspring values) have smaller standard errors than sib-sib estimates. The effects of dominance and a common environment will inflate sib-sib heritability estimates, whereas maternal effects (operating pre- and post-natally) may increase mother-offspring values, so that father-offspring heritabilities are generally regarded as the most reliable.

Twin studies, although they estimate broad heritability (and Falconer (1981) suggests that this may be the more appropriate index with human data), are probably less biased from the effects of the common environment than sib-sib studies. However, they are based on the following assumptions:

1) That both types of twins (mono- and dizygotic) are subject to the same type of environmental conditions.

2) That the total genetic variance is the same in the two types. Corruccini et al. (1986) found unequal variance in monozygotic and dizygotic twins in a study of dental occlusal and arch variables.

3) That the heritability estimates will apply to non-twin populations. Nance (1976) found that the rates for dizygotic twinning varied in different races, whereas monozygotic rates were uniform. This suggests that monozygotic twins may represent a particular stratum of the population.

Falconer (1981) suggests that where the total variance of twins is not the same as that of singletons, the heritability estimated from singleton pairs, despite the high standard error, may be more applicable to the general population. Kang et al. (1977) proposed a method of partitioning genetic variance estimated from twin data into environmental and dominance components, using several estimation procedures. They recommended the use of this weighted estimate whenever the total variance of the two types of twins was not equal, cautioning that "until the magnitude of dominance and the degree of environmental covariance can be ascertained, the accuracy of heritability estimates obtained from twin data will be questionable."

Assortative mating, expressed as the phenotypic correlation between the parents, is a further source of error in family studies. If the phenotypic correlations reflect correlated 'breeding values', then the additive variance and hence the heritability will be inflated. This effect can be overcome by using the mid-parent values, provided the phenotypic variances are the same in both sexes.

Family and twin studies have been undertaken by many workers for metric traits, using cephalograms or measurements taken on the living. Since few non-metric traits can be identified from radiographs, the majority of workers investigating non-metric traits in man have concentrated on dental traits. Skeletal series from mice and macaques have also been examined. The calculation of heritability estimates from non-metric traits is complicated by the fact that categorical data must be transformed into normally distributed variables. Self and Leamy (1977) used three methods to overcome this difficulty:

1) Pooling both sides of both parents to obtain five phenotypic classes which are then subject to an arcsin angular transformation (Snedecor and Cochran 1973) to produce a near normal distribution.

2) Using the maximum likelihood correlation between offspring and parent (Tallis 1962, Mendell and Elston 1974). This postulates an underlying bivariate normal model with thresholds imposed upon it to give discrete classes. The parameters of the model are chosen to give the best possible fit with the observed values, and the model is then used to calculate the correlations.

3) Using Falconer's (1965) method where 'trait liability' is the underlying normally distributed variable from which the correlations are derived. The trait incidence represents the area under the curve beyond the threshold.

Of the above methods, Falconer's has been the most commonly used in this field. This model is inadequate if the liability is not multifactorial and unimodal, which might be the case if a major gene were affecting the trait. Falconer (1981) advises caution in the use of discontinuous traits in heritability studies:

> . . . threshold characters do not provide ideal material for the study of quantitative genetics, because the genetic analyses to which they can be subjected are limited in scope and subject to assumptions that one would be unwilling to make except under the force of necessity.

2.2. Family studies - a review.

2.2.1. Metric traits.

In the consideration of cranial metric traits, an important question arises, namely, what is the appropriate unit of study? It is generally accepted that growth patterns are hereditary (Krogman 1967), but, as Kraus et al. (1959) point out, the craniofacial complex *is* a complex, and:

> There is no gene or group of genes whose primary effect is to achieve a certain length of bone, a certain angle or a given morphology. In fact, with very few exceptions, primary effects of genes are not known.

Sperber's (1981) account of the factors which determine the eventual size and shape of the cranial vault illustrate the complexity of the growth patterns. In the fetal and infant skull

the expanding brain exerts separating tensional forces on the sutures, secondarily stimulating growth at these points. After the age of four years, surface apposition becomes more important, intracranial pressure affecting the inner table of compact bone and external muscular forces the outer table. Growth in the inner and outer layers is somewhat independent, as is shown by the thinning of the vault in hydrocephaly.

Enlow et al. (1971) stressed that any bony part must have a geometric or architectural counterpart to which its growth pattern must be matched if "the same overall proportionate structural configuration is to be sustained." Van Limborg (1970) found that in the normal situation, face and vault growth were controlled by few intrinsic genetic factors but that local environmental tensional factors were of great importance.

Stein et al. (1956) recommended the comparison of angles and measurements involving localised sectors of the skull in radiographic family studies, as these areas "might be expected to show hereditary resemblances more consistently than those involving larger or more widely separated sectors". Kraus et al. (1959), in a study of six sets of same-sexed triplets, attempted to determine "if the craniofacial complex, either as a whole or in its component parts, is under the discernible control of heredity". They examined tracings taken from frontal and lateral cephalograms for concordance, and related this to the zygosity determined from a battery of tests. With the whole lateral film, they found no correlation between concordance and zygosity; one set of trizygotic triplets showed as much concordance as the monozygotes. Their conclusions were similar for the vault and face considered separately. They then examined tracings of seventeen single bone profiles and found almost perfect concordance in the monozygotic triplets and a low degree of concordance (less than 50%) in the di- and trizygotic sets. They concluded that:

> The utility of diameters and angles, which are in reality simply mental constructs, for recognizing the inheritance factor is brought into serious question.

This conclusion may, however, be too pessimistic. Nakata et al. (1976) investigated lateral radiographs of families (including twins) and formulated an overall shape dissimilarity parameter d_h, for use in comparisons, rather than a subjective assessment of concordance. Anatomical points on the cephalograms were marked and transformed into

Cartesian coordinates. Coordinate pairs were then centred, rotated and reduced in size until the squared distances between homologous points were minimised. Carefully controlling for error, they found that monozygotic twins had the least dissimilar outlines, followed by dizygotic twins, sib pairs and finally husband-wife pairs. All group means were significantly different; the variances of d_h also followed the same rank order.

The majority of family studies have employed standard cephalometric or anthropometric measurements. Some of the measurements bear little relationship to conventional cranial metrics, and in the following review, special emphasis is placed on those results which are directly applicable to the measurements employed in this study. These measurements, and their craniometric equivalents, are indicated in tables 2.1 to 2.4.

Vandenberg (1962) reviewed six anthropometric twin studies, comparing the F-values for each measurement. The F-value is calculated as follows:

$$F = Var(DZ) / Var(MZ),$$

where Var(DZ) and Var(MZ) are the intra-pair variances for dizygotic and monozygotic twins respectively. The variance of dizygotic twins has environmental and genetic components; that of identical twins represents environmental effects only. Vandenberg found that the six studies consistently showed a significant genetic component to the variance. The results for cranial measurements from 4 of those studies (Clark 1956, Vogel and Wendt 1956, Osborne and De George 1959, Vandenberg and Strandskov 1964) are reproduced in table 2.1. Clark (1956) also calculated heritability (broad heritability) values for each trait, and these are shown in table 2.2, along with parent-offspring (narrow heritability values) calculated by Susanne (1977). Clark's estimates are all highly significant ($p < 0.01$) and support the concept of a sizeable genetic component in the variances of these measurements. Susanne uses Fisher's heritability estimate which compensates for assortative mating, and all values are significant except for nasal height, the low value of which is attributed to measurement error caused by the difficulty of locating nasion in the living subject.

Familial correlations have been frequently studied. Brown (1973) examined lateral radiographs from forty-five Irish families and found overall significant and high

TABLE 2.1

F-RATIOS OF HERITABILITY FROM 4 TWIN STUDIES.

(MODIFIED FROM VANDENBERG 1962)

	Clark (1956)	Vogel and Wendt (1956)	Osborne and De George (1959)	Vandenberg and Strandskov (1964)
Head length	2.18**	5.33**	0.76	3.23**
Head breadth	3.58**	2.68**	6.18**	3.70**
Head height	3.19**	-	0.83	1.13
Frontal breadth	2.61**	4.88**	2.07**	2.00**
Bizygomatic breadth	2.49**	3.07**	1.88*	5.80**
Total face height	3.75**	8.03**	2.76**	2.92**
Upper face height	3.62**	-	3.34**	-
Nose height	4.19**	5.83**	3.65**	1.78*
Nose breadth	2.95**	2.67**	2.81**	3.75**

* - $p < 0.05$

** - $p < 0.01$

The following anthropometric and cranial measurements are roughly equivalent:

Head length	- GOL	Upper face height	- NPH
Head breadth	- XCB	Nasal height	- NLH
Bizygomatic breadth	- ZYB	Nasal breadth	- NLB

TABLE 2.2

HERITABILITY ESTIMATES FROM TWIN AND FAMILY STUDIES.

	Clark (1956) Twins	Susanne (1977) Parent-child
Head length	.54	.55
Head breadth	.72	.61
Head height	.69	.72
Frontal breadth	.61	.67
Bizygomatic breadth	.60	.61
Total face height	.74	.58
Upper face height	.72	.52
Nasal height	.76	(.39)
Nasal breadth	.66	.64

Heritabitity estimates in parentheses are not significantly different from zero.

The following anthropometric and cranial measurements are roughly equivalent:

Head length	- GOL	Upper face height	- NPH
Head breadth	- XCB	Nasal height	- NLH
Bizygomatic breadth	- ZYB	Nasal breadth	- NLB

correlations for the chords, subtenses and angles of the frontal and occipital bones, and for cranial length and nasal height. Children were found to derive their similarities from both parents, but were more similar to the parent of the same sex.

Table 2.3 presents the correlation estimates for brothers taken from four studies (Howells 1953, 1966b, Susanne 1975, Poosha et al. 1984). For sib pairs the correlation is not expected to exceed 0.5, but in practice this often occurs. Ethnic heterogeneity (Howells 1953), as well as common environmental effects may inflate the values. Howells used only adult brothers in his study whereas Poosha et al. and Susanne used age-standardised variables from adults and children. Head length and breadth have significant and high values in all four studies, as have bizygomatic breadth and minimum frontal breadth. Nose height is consistently more heritable than width, though Susanne (1975) finds both values non-significant in his study.

Howells (1953) and Susanne (1975) in the same studies noted that longitudinal body measurements had very high heritabilities compared to widths and circumferences. Longitudinal growth in the long bones is almost entirely due to growth at the cartilaginous metaphyses. Van Limborgh (1970) found that "the growth of the chondrocranium is almost exclusively governed by intrinsic genetic factors" and Sperber (1981) points out that the chondrocranium is phylogenetically the oldest, most stable part of the cranium. Nasal height is primarily the product of septal cartilage growth, which is part of the chondrocranium, and this may account for the high heritability of nasal height compared to breadth.

Multivariate techniques have been used in family studies by Howells (1953) and Nakata et al. (1974). The rationale for their use is that craniofacial measures have been previously treated as independent variables, despite the fact that they are obviously interrelated.

> Since it is possible that genetic and environmental factors influence multiple craniofacial measurements in a complex manner, an analysis of the correlations among these measurements would seem to be a more logical and reasonable approach to understanding the inheritance of those interrelated characters. (Nakata et al. 1974)

TABLE 2.3

FAMILIAL CORRELATION COEFFICIENTS FOR MALE SIB PAIRS.

	Howells (1953)	Howells (1966b)	Susanne (1975)	Poosha et al.(1984)
Head length	.41	.40	.36	.39
Head breadth	.56	.42	.37	.46
Head height	.48	-	-	-
Total face height	.66	-	.52	-
Upper face height	.54	-	.33	-
Frontal breadth	.55	.34	.41	.48
Bizygomatic breadth	.44	.31	.45	.48
Nose height	.56	.48	(.19)	.52
Nose breadth	(.18)	.22	(.00)	.39
No. of pairs	76	683	102	200-500

Correlation coefficients in parentheses are not significantly different from zero.

The following anthropometric and cranial measurements are roughly equivalent:

Head length	- GOL	Upper face height	- NPH
Head breadth	- XCB	Nasal height	- NLH
Bizygomatic breadth	- ZYB	Nasal breadth	- NLB

Nakata et al. (1974) measured thirty-three cranial variables from cephalograms of twin and sib families and obtained nine factors each related to an area of the skull. Mid-parent-offspring heritability estimates ranged from 0.31 to 0.57 and all values were significant. Estimates derived from twins ranged from 0.31 to 0.76, exceeding the parent-offspring values for some factors but not for others, which suggests that dominance effects are not present in all factors. Factor heritabilities generally fell within the range of the individual heritability values of the variates with the highest loadings.

The difficulties involved in the interpretation of standard heritability and correlation estimates have led more recent workers to adopt the method of path analysis, first developed by Wright (1921) and extended for the study of nuclear family data by Rice et al. (1978). Path analysis attempts to account for the pattern of familial correlations with various models; the correlations generated by these models are then tested for 'goodness of fit' to the original data with likelihood ratio tests. It has the advantage that transmission between generations need not consist of genetic factors alone; cultural inheritance can be included, and common environmental effects and assortative mating can enter the model and be controlled for, rather than being regarded as a source of error in the derived heritability estimates.

Sharma at al. (1984) and Byard et al. (1984) studied anthropometric traits in a Punjabi community, using families containing twins and singleton births. Sharma et al. calculated correlations using the maximum likelihood method of Rao et al. (1982) which compensates for the overestimate of sample size which occurs when all possible pairs of relatives are used. They found that marital correlations were high for body measurements, but not for head or face variables. Twin correlations were higher than those derived from other family members, as expected from theoretical considerations. No significant sex effects were found, apart from maternal effects.

Byard et al. (1984) submitted these correlations to path analysis to test various models of inheritance. Transmissibility (t^2), the proportion of the phenotypic variance explained by transmissible factors (genetic and cultural) was thus calculated. The values (shown in table 2.4) were generally high (greater than 0.6) except for head height, and

TABLE 2.4

TRANSMISSIBILITY COEFFICIENTS DERIVED FROM PATH ANALYSIS.

	Most parsimonious model.		Genetic transmission only.	
	Poosha et al. (1984)	Byard et al. (1984)	Byard et al. (1984)	Devor et al. (1986)
Head length	.68	.61	.61	.44
Head breadth	.34	.76	.65	.57
Head height	-	.29	.29	-
Frontal breadth	.51	.72	.70	.28
Bizygomatic breadth	.42	.62	.67	.40
Facial height	.67	.92	.70	.40
Upper facial height	-	-	-	.57
Nasal height	.44	.93	.62	.51
Nasal breadth	.39	.71	.73	.38

All estimates are significantly different from zero.

The following anthropometric and cranial measurements are roughly equivalent:

Head length	-GOL	Upper face height	-NPH
Head breadth	-XCB	Nasal height	-NLH
Bizygomatic breadth	-ZYB	Nasal breadth	-NLB

were generated both for the most parsimonious model, and with the constraint of genetic factors being the only form of transmission between generations.

By setting the path factors to predetermined values, hypotheses could be tested; a transmission factor of 0.5, for example, implies pure polygenic autosomal inheritance. The hypothesis of no familial transmission was rejected for all variables and no assortative mating was found for cranial measurements. Twins showed common environmental resemblances except for head breadth, nasal height and facial length. Maternal effects were absent, except for minimum frontal breadth, and there were no departures from polygenic inheritance, except for facial length and jaw height.

Poosha et al. (1984) also used path analysis in a study of craniofacial measurements in non-twin families from Andra Pradesh. Their transmissibility estimates (for the most parsimonious model), included in table 2.4, were generally lower than those of Byard et al. They confirmed Brown's (1973) finding that familial correlations are higher in same-sexed pairs. Head length was found to be consistent with a simple polygenic model of inheritance, and highly heritable, but breadth measurements, total face height and nose measurements were affected by other factors, such as marital resemblance, cultural inheritance and common sibling environment.

Devor et al. (1986) in a study of Mennonites from Kansas and Nebraska found that transmissibility estimates for cranial measurements ranged from 0.4 to 0.6 (see table 2.4). They attributed the higher estimates reported by Byard et al. (1984), where values lie almost exclusively above 0.6, to the inclusion of twin data in that study. Devor et al. found evidence of assortative mating only for morphological facial height and residual sibling effect was absent for all cranial measurements.

To conclude, it is difficult to make definitive statements regarding the heritability of any particular measurement, as the works reviewed often provide conflicting evidence. However, the following points may be noted:

1) It is clear that there is a significant genetic component in the variance of many skull measurements, though the magnitude of the component is difficult to define. Keita

(1983), from a review of the literature, considers the following measurements to be predominantly inherited:

Cranial length	Nasal height
Cranial breadth	Nasal breadth
Minimum frontal breadth	Basion-nasion length
Bizygomatic breadth	Upper facial height
Biauricular breadth	

To these could be added the sagittal vault chords, subtenses and angles utilized by Brown (1973).

2) Measurements related to the cranial base are probably more heritable than others (Van Limborgh 1970); these include Howells' biauricular breadth and, owing to its correlation to base width (Howells 1973, Schulter 1976), maximum cranial breadth. It is interesting to note that Howells (1973) found cranial and basal breadths to be his most important population discriminators. Nasal height could also be included in this group, as it is related to the cartilaginous nasal septum.

3) As workers have failed to demonstrate unequivocally an absence of sex factors in trait heritability, the sexes should be separated prior to metric analysis.

4) Measurements relating to a single bone are more likely to reflect inheritance than ones crossing several complex regions.

2.2.2. Non-metric traits.

Few human studies have been undertaken to assess the heritability of non-metric traits. Research is complicated by the lack of suitable skeletal family series, so that evidence for the genetic basis of these traits comes mainly from mice (Grüneberg 1963, Self and Leamy 1978) and macaques (Cheverud and Buikstra 1981, 1982). Since few non-metric traits can be identified from radiographs, most family studies have utilized dental traits. These will be briefly reviewed since, although they are not utilized in the present work, they present evidence that discrete traits have, in general, a genetic basis.

Minor variants of the dental crown have been observed to vary in frequency from population to population and have been included in many racial studies (Scott 1980, Berry 1978, Brewer-Carias et al. 1976, Sofaer et al. 1972). They are easily scored in the living

from dental casts. Dahlberg (1971) stressed the advantage of dental traits over bony ones for determining population affinities:

> Once the calcification of a crown is completed, tooth form can be changed only by . . . abrasion and wear. Bone, on the other hand, is responsive to pressures and environmental impacts which result at times in considerable remolding and new adaptation.

Berry (1976) cautions, however, that since caries or attrition tend to be almost universal, the usefulness of dental traits in population studies is severely limited.

Kraus (1956) considered that crown patterns, the presence of cuspules, ridges, wrinkles and pits, shovel-shaped incisors and incisor rotation had a genetic basis. Sofaer et al. (1972) and Goose and Lee (1971), finding that familial correlations for traits and tooth size respectively varied in different populations, cited this as evidence of the presence of environmental factors, as did Kolakowski et al. (1980) to explain higher sib-sib correlations compared to parent-offspring values. These differences could, however, equally well be caused by genetic factors, as noted in section 2.1.

The nature of the genetic influence on tooth morphology is also controversial. Kraus (1951) studied Carabelli's cusp in eight family pedigrees, concluding that a major gene effect was indicated. Goose and Lee (1971), however, tested simple genetic models for the same trait and found a poor fit, suggesting instead a multifactorial inheritance. Portin and Alvesalo (1974) were unable to distinguish between a single locus or a polygenic model in a family study of shovel-shaped incisors. Lee and Goose's (1972) analysis of familial correlations in a Chinese immigrant and a local population in Liverpool led them to conclude that simple Mendelian inheritance was an unacceptable hypothesis for shovel-shaped incisors, number of molar cusps and mandibular molar fissure patterns.

It is possible to detect some skeletal traits in radiographs. Torgersen (1951a, b), in a study of metopism and wormian bones in the lambdoid suture in Norwegian families found familial concentration in both traits. He concluded that metopism was the result of a dominant gene showing incomplete penetrance, and that both features were controlled by genes which delay suture closure generally and other genes which influence the location of ossification centres. Selby et al. (1955) found a higher incidence of posterior atlas bridging

in the relatives of affected individuals (and a lower incidence in relatives of those unaffected) when compared to the general population. Saunders and Popovich (1978) confirmed these findings for atlas bridging, found highly significant correlations between parents and offspring and sibs, no evidence of maternal effects or assortative mating and also showed that the results were consistent with a quasi-continuous polygenic model of inheritance (Grüneberg 1963). Their results were similar for clinoid bridging, though correlations were less significant and major gene effects on the trait could not be ruled out.

Self and Leamy (1978) investigated the heritability of cranial traits in a random-bred population of house mice. The values obtained were generally low but this could be accounted for by the group's recent emergence from an inbred strain. The amount of additive variance found in the discrete traits was close to that expected under a polygenic model due to an accumulation of mutations in the fifty-two generations since the emergence of the strain (Self and Leamy 1978).

Cheverud and Buikstra (1981) studied a skeletal series of rhesus macaques to estimate the heritability of trait liability, using Falconer's method. Heritability estimates ranged from -0.22 to 1.12 (though no value was significantly less than zero or greater than one), and half of the fourteen traits had a value greater than 0.5. They found that estimates for hyperostotic and hypostotic traits (Ossenberg 1970) were larger than those for traits scoring the number of foramina. In a later paper (Cheverud and Buikstra 1982) they compared heritability estimates in the same series for both metric and non-metric traits, finding that the latter had significantly higher values. The fifty-six metric variables had an average heritability of 0.32 and the fourteen non-metric traits, 0.53. When hyperostotic traits and foraminal traits were considered separately, the heritability estimates for foraminal traits (h^2 =0.35) were not significantly larger than those for the metric variables, but hyperostotic traits had a very high average heritability (h^2 =0.80).

In conclusion, although direct evidence concerning the heritability of most osseous non-metric traits in man is lacking, numerous animal studies and dental studies have suggested that a strong genetic component is present in at least some of them. These traits

are, however, of many different types and generalisations regarding them may not be justified. The degree of genetic determination of any one trait may depend on its type, or its mode of development (Cheverud and Buikstra 1982). With this in mind, section 4.2.2 reviews each trait in turn, discussing the evidence for a genetic or environmental aetiology.

2.3. The contribution of hybrid studies.

2.3.1. Metric traits.

Sibling correlation and heritability estimates, for reasons noted earlier, are difficult to interpret. A consideration of skull morphology in hybrid groups can greatly facilitate the understanding of the genetic basis of these features. It has long been appreciated that cranial measurements show different mean values in some racial groups (Woo and Morant 1934, Allbrook 1958, Giles and Elliot 1962) so that the study of hybrids formed from widely separated racial groups can help validate or invalidate the conclusions derived from family studies (Keita 1983). These studies also fit well the model used in interpreting genetic distances between populations i.e. that distances reflect the degree of genetic similarity derived from common ancestry.

Hybrid studies assume the polygenic, equally-additive inheritance of morphological features (Corruccini et al. 1982). This assumption may not be correct, as the phenomenon of heterosis (hybrid vigour) demonstrates. Heterosis has been shown to increase the mean values and variance of phenotypes in F1 crosses in many plant and animal studies; conversely, these are reduced in highly inbred lines (Falconer 1981). It is a matter of controversy as to whether these effects can be seen in man. Trevor (1938), assessing cranial measurements in nine hybrid series, found that where there was a clear distinction between means in the parent groups, hybrid mean values were intermediate and the variances were not, on the whole, different from those of the parent groups. Howells (1966b), looking at anthropometrics in a highly inbred religious isolate, could not demonstrate the expected decrease in variance.

Strouhal (1971), however, found an increase in metric means paralleling levels of exogamy in inbred Nubian villages though the cranial increases were not significant.

Krishnan (1986), analysing anthropometrics in the children of consanguinous and unrelated parents in Delhi Muslims, showed a slight but significant decrease in the mean values for all measurements in the inbred group. He did not consider variance, but this can be calculated from the standard error of the mean, which is shown in the tables; for the cranial measurements, the variances of the outbred groups were not significantly greater (one-tailed F-test) than those of the inbred groups (except in one case where the very low value of the S.E.M. suggests a typographical error).

2.3.2. Non-metric traits.

Epigenetic traits have also been studied in hybrid groups. Wijsman and Neves (1986) compared gene frequencies in Brazilian Blacks, Whites and Mulattos, and contrasted the frequencies of traits in crania of known origin from a medical collection. Although the sample of Mulatto skulls is small (28) they point out that it is in the same range as other populations from which trait-based genetic distances have been derived. They found that gene frequencies in Mulattos were intermediate between those of the black and white 'parent' populations, which result is highly compatible with a linear model of gene admixture. Very few traits, however, showed a similar phenomenon; in fact, the distances between Blacks and Whites were frequently smaller than those between either group and the Mulattos.

Corruccini et al. (1982) examined non-metric dental and cranial traits in a 17th to 19th Century slave population, and compared them with frequencies in modern American Blacks (the hybrid group) and Whites . Admixture rates derived from traits were found to be much higher (39% for dental and 75% for cranial traits) than the 10% to 20% figures derived from genetic marker studies.

In summary, Trevor's (1938) results suggest that in hybrid studies, cranial measurements provide a more reliable indicator of genetic similarity than do epigenetic traits. Wijsman and Neves (1986) point out that the mode of inheritance of these traits is poorly understood and that dominance, threshold effects and environmental influences would result in deviation from the expected colinearity. They conclude:

> ... distance measures based on such traits bear at most a weak relationship to distance measures based on gene frequency data only (which) implies that conclusions about relative degrees of genetic similarity made on the basis of discrete-trait data must be made cautiously.

2.4. Comparative distance studies.

Many workers have attempted to assess the value of morphological distances by comparing them with other measures of distance derived from the same populations. These alternative measures may be based on non-biological criteria (e.g. geographic, linguistic, historical or cultural), or on biological ones such as blood group frequencies, dermatoglyphics and odontometrics. Although only the biological comparisons can reveal the degree of correspondence between morphological and genetic distances, the first type of study tests the practical value of the morphological distance for the elucidation of population origins and migrations.

Most studies have concentrated on metric variables, since these can readily be studied in living subjects, for which serological and dermatoglyphic, as well as non-biological data is available. Less commonly, non-metric traits have been studied (usually in conjunction with metric ones) in skeletal populations, and the results compared with linguistic-historical interpretations. Dental non-metric traits have also been studied in the living.

In assessing the results of this type of study, it should be emphasised that the method of comparison of the distances varies. This ranges from visual inspection of the distances, plots or trees (Rightmire 1972) to complex statistical methods. Relethford and Lees (1982) discuss the merits of the various methods used. Five such methods can be identified:

1. A correlation coefficient between all pair-wise elements of two distance matrices may be computed. This method has been used in several studies (e.g. Friedlaender et al. 1971, Howells 1966c, Brooks and Van Arsdale 1964, Hanna 1962), but the Pearson product-moment correlation coefficient is inappropriate since:

   a) it assumes that the elements of the matrix are independent; though this may be true for matrices of MMDs, it is not the case with matrices of Euclidian distances such as D^2.

b) it assumes bivariate normality of the variates.

c) it assumes a linear relationship.

Nonparametric rank-order correlation statistics, such as Spearman's *rho* or Kendall's *tau* are more suitable, since they avoid the assumptions of normality and linearity (but not monotonicity), although the problem of interdependence remains. Nonparametric correlations have been used by Neel et al. (1974), Spielman (1973) and Rothhammer and Spielman (1972), among others.

2. Dendrograms derived from several distance matrices may be compared. This method has been successfully used in a number of studies (e.g. Neel et al. 1974, DaRocha et al. 1974, Spielman 1973, Friedlaender et al. 1971), but the method is complicated and gives results similar to other simpler methods.

3. If the distances are represented by plots of points in space, two plots can be compared using the technique of Procrustes analysis, developed by Gower (1971). This method is essentially the same as that of Schönemann and Carroll (1970), involving the rotation, reflection and scaling of the plots until the discrepancies between homologous points are minimised. A statistic which measures the degree of correspondence between the plots is also produced. It has a value between 0 and 1, the former denoting a perfect fit, but general significance tests for this statistic have not yet been developed. This method has been used in several studies of quantitative traits (e.g. Neel et al. 1974, Relethford et al. 1981).

4. A recently developed technique, known as quadratic assignment (Dow and Cheverud (1985), based on a method originally proposed by Mantel (1967)) directly compares distance matrices, and can be used to determine which of two matrices most closely corresponds to a third. Dow and Cheverud used it to re-analyse earlier work on populations from Venezuela (Spielman 1973) and Bougainville (Friedlaender 1975).

5. Several studies have suggested extensions to simple correlation analysis. Recognising that non-biological matrices are often intercorrelated, Rothhammer and Spielman (1972) used partial correlation and path analysis to partition intercorrelations of distance measures based on anthropometrics, geography and altitude. Dow et al.

(1987) outlined an approach to partialling distance matrices which produced well-defined coefficients and valid significance tests.

Because of the different methods in use, the rigorous comparison of results between studies is difficult. Fortunately, most of the works present biological distance matrices, from which a correlation coefficient can easily be calculated; geographic distances are less often presented, but straight-line distances can be taken from the accompanying maps. In the following review, Spearman's rank order (*rho*) correlation coefficients have been calculated whenever feasible, to aid in the evaluation of the studies.

2.4.1. Comparative studies involving metric traits.

Anthropometrics and non-biological distances.

One of the commonest non-biological distances employed is geographic distance. This is studied in relation to genetic distance on the hypothesis that large distances act as a barrier to gene flow. Anthropometrics have shown a moderate to good congruence to geographic distance in a number of studies (e.g. Neves et al. 1985, Pingle 1984, Neel et al. 1974, DaRocha et al. 1974, Spielman 1973, Chai 1972, Howells 1966c). Table 2.5 lists the correlations found in some of these studies.

Straight-line geographic distance may not, however, be a reliable guide to the degree of genetic isolation. Hiernaux (1972) found a poor correspondence between anthropometric variables and geographic distance in tribes from Rwanda and Burundi. He noted, however, that caste and ethnic boundaries were the most important factors acting on gene flow, and geographic distance was largely irrelevant. Similarly, correlation coefficients derived from Chai's (1972) data (see table 2.5) suggest a poor correspondence, but the author's comments on the terrain of Bougainville Island reveal that apparently close groups may be separated by impassable mountains. Chai, in fact, considers that his anthropometric distances correspond well to the degree of geographic isolation.

Distances based on archaeological, cultural and linguistic differences may provide a better indication of genetic isolation than geography. Dow et al. (1987) state that:

TABLE 2.5

CORRELATIONS BETWEEN ANTHROPOMETRIC AND

GEOGRAPHIC DISTANCE MATRICES.

Study	Correlation coefficient product-moment	rank-order
Howells (1966c)		
18 Bougainville groups	.24	-
Rothhammer & Spielman (1972)		
6 Aymara groups (Peru)	-	.69
Chai (1972)		
8 Taiwan tribes	-	(.25)
Spielman (1973)		
19 Yanomamo villages	-	.80
7 Yanomamo villages	-	.73
Neel et al. (1974)		
7 Yanomamo villages	-	.29
Da Rocha et al.(1974)		
7 S. American villages	-	.64*
Froehlich & Giles (1981)		
9 Papuan villages	-	.72
Dow & Cheverud (1985)		
18 Bougainville villages	(.17)	-
19 Yanomamo villages	.84	-
Dow et al. (1987)		
8 Solomon Islands groups	(.25)	-
Relethford (1988)		
5 Irish groups	.72	-

Figures in parentheses are not significant.

All other values are significant ($p < 0.05$); however, with the exception of the results of Dow and Cheverud (1985), Dow et. al (1987) and Relethford (1988), the tests of significance may be inappropriate since the distance values on which the matrix correlations are based are not independent.

* - coefficient calculated from results given in the study.

> geographic distances relate to the magnitude of gene flow . . . (while) the magnitude of linguistic differentiation, especially after effects due to proximity are removed, is directly related to time since divergence, . . .

Several studies have shown that anthropometrics have a moderate to good congruence with linguistic, historical-linguistic and geographic-linguistic distances e.g. Ossenberg (1977), Zegura (1975), Rightmire (1972), Friedlaender et al. (1971), Howells (1966c) and Hanna (1962). Neves et al. (1985), however, found that language type was poorly reflected in a principal components analysis of anthropometric data from Brazilian Indians. The results of some of these studies are shown in table 2.6.

Other non-biological measures of distance have occasionally been used. El-Najjar (1978) and Sphuler (1954) examined anthropometric data on several Indian groups from Arizona and New Mexico, and found that they agreed well with the historical, ethnographic and cultural conclusions. Dow and Cheverud (1985) report a good correspondence between migration matrices and anthropometric distances for data from 18 Bougainville villages.

Anthropometrics and biological distances.

A number of studies have focused on the relationship between anthropometrics and other measures of biological distance. This type of study is founded on the hypothesis that:

> . . . (a) distance matrix based on one set of (genetic) characters will, within limits set by the sampling process and the environmental contribution to the phenotype, correspond to a similar matrix based on a different set of characteristics.
> (Neel et al., 1974)

The vast majority of these studies have employed distances based on data from red cell and serological typing - a 'true' genetic distance. A few workers have employed dermatoglyphic distances (Neel et al. 1974, Chai 1972), since dermal ridge counts are thought to be almost entirely under genetic control. The development of palm and finger ridges is complete by the fourth month of fetal life, and thereafter they cannot be altered by environmental forces. Heritability for ridge-counts in fingers (Holt 1953, Bonnevie 1924) and palms (Glanville 1965, Pons 1964) are close to 100%, and Dow et al. (1987) have shown that dermatoglyphics are of great value in assessing local historical relationships among groups from the Solomon Islands.

TABLE 2.6

CORRELATIONS BETWEEN ANTHROPOMETRIC AND LINGUISTIC DISTANCE MATRICES.

Study	Correlation coefficient: product-moment	Correlation coefficient: rank-order
Howells (1966c)		
18 Bougainville groups	.43	-
Ossenberg (1977)[+]		
5 Eskimo groups - male	-	(.50)
5 Eskimo groups - female	-	.75
Dow & Cheverud (1985)		
18 Bougainville villages	.55	-
Dow et al. (1987)		
8 Solomon Islands groups	(.09)	-

Figures in parentheses are not significant.

All other values are significant ($p < 0.05$); however, with the exception of the results of Dow and Cheverud (1985) and Dow (1987) the tests of significance may be inappropriate since the distance values on which the matrix correlations are based are not independent.

[+] Ossenberg used the F-values of the Mahalanobis distances rather than the distances themselves.

Table 2.7 shows the results of several studies which compare anthropometric and marker-gene distances. In general they show a moderate to good correspondence, which implies that measurements have a significant genetic component. Dermatoglyphic comparisons (see table 2.8), conversely, have shown only a moderate to poor correspondence (Neel at al. 1974, Chai 1972). This may reflect the differing evolutionary forces which act on these traits, since dermatoglyphics are thought to be affected by genetic drift alone, whereas anthropometrics are also responsive to selective pressures (Chai 1972).

2.4.2. Comparative studies involving non-metric traits.

Cranial non-metric traits have been the subject of relatively few comparative studies. Most of these have utilised skeletal populations and compared both metric and non-metric distances to non-biological distance measures. A few workers have compared discrete dental traits from living populations to geographic and marker gene distances.

Non-metric traits in skeletal populations.

One of the earliest studies was undertaken by Laughlin and Jørgensen (1956). They contrasted metric and non-metric distances in the crania of four populations of Greenlandic Eskimo. Utilising a variant of Penrose's size and shape statistic, the coefficient of divergence, they found that both the metric and the non-metric distances reflected the known pattern of coastal migrations.

Rightmire (1976) studied crania from 6 African tribes, comparing the results from metric (Mahalanobis' D^2) and non-metric (Sanghvi's Chi-square distance) analyses to a tree derived from archaeological, linguistic and other non-biological information. He found that the distances derived from metric traits reflected much more closely the pattern of relationship suggested by the non-biological criteria. Zegura (1975) undertook a similar study on crania from 12 groups of North American and Greenlandic Eskimo crania, using Sanghvi's B^2 for the non-metric traits. He too concluded that metric distances agreed more closely with linguistic patterns of relationship than did the non-metric ones.

Conversely, in Ossenberg's (1977) study of crania from five Alaskan populations, non-metric trait distances were found to correspond more closely with the non-biological picture

TABLE 2.7

CORRELATIONS BETWEEN ANTHROPOMETRIC AND

SEROLOGICAL DISTANCE MATRICES.

Study	Correlation coefficient product-moment	Correlation coefficient rank-order
Sanghvi (1953)		
5 Bombay groups	-	.69*
Pollitzer (1958)		
4 white & negro groups	-	1.00*
Hiernaux (1956)		
15 African groups	.63	-
Rothhammer & Spielman (1972)		
6 Aymara groups (Peru)	-	(.33)
Spielman (1973)		
19 Yanomamo villages	-	(.19)
7 Yanomamo villages	-	(-.25)
Neel et al. (1974)		
7 Yanomamo villages	-	.30
DaRocha et al. (1974)		
8 S.American villages	-	.44*
Froehlich & Giles (1981)		
9 Papuan villages	-	.64
Pingle (1984)		
5 Gondi tribes - male	-	(.48)*
5 Gondi tribes - female	-	.58*
Dow & Cheverud (1985)		
18 Bougainville villages	.42	-
19 Yanomamo villages	(.11)	-

Figures in parentheses are not significant.

All other values are significant ($p < 0.05$); however, with the exception of the results of Dow and Cheverud (1985) the tests of significance may be inappropriate since the distance values on which the matrix correlations are based are not independent.

* - coefficient calculated from results given in the study.

TABLE 2.8

CORRELATIONS BETWEEN ANTHROPOMETRIC AND DERMATOGLYPHIC DISTANCE MATRICES.

Study	Correlation coefficient: product-moment	Correlation coefficient: rank-order
Chai (1972) 8 Taiwan tribes	-	.32*
Neel et al. (1974) 7 Yanomamo villages	-	(.08)
Froehlich & Giles (1981) 9 Papuan villages	-	.66

Figures in parentheses are not significant.

All other values are significant ($p < 0.05$); however, the tests of significance may be inappropriate since the distance values on which the matrix correlations are based are not independent.

* - coefficient calculated from results given in the study.

of relationships. Ossenberg used the F-value of D^2 and a modified form of the Grewal-Smith MMD for metric and non-metric traits respectively. She found that the MMDs (from a pooled sex group) and the F-values derived from females were both highly correlated (using Spearman's rho) with the linguistic-geographic interpretation, but that F-values derived from males were not significantly correlated with the non-biological results.

Berry (1974) collected data on non-metric trait frequencies in 21 samples of crania from Scandinavia, Iceland and the British Isles. She analysed the resulting distances and found that, in general, the trends shown were compatible with the known population movements.

Rothhammer et al. (1982, 1984) compared metric and non-metric distances to a measure of chronological distance. They studied five prehistoric groups from the coastal region of Northern Chile, representing "samples taken from the same population at different stages of its micro-evolutionary history" (Rothhammer et al. 1982). Using Sanghvi's Chi-square and MMD as measures of non-metric distance, they found good correlation with chronological distance (product-moment r = .83 and .75 respectively). Metric (D^2) distances also corresponded well (r=.84) with chronology, and there was good agreement between the two non-metric measures and metric distances (r = .85 in each case).

Non-metric traits in living populations.

Sofaer et al. (1972) recorded the incidence of 10 dental traits in three tribes from south-western India. They found that when all 10 traits were considered, the two tribes most similar genetically and geographically were most dissimilar dentally. Reducing the number of traits utilized led to a better correspondence with genetic and geographic distance, but the results of this study are of little value since three inter-group distances are an insufficient number for comparison.

Dental non-metric traits were also examined by Brewer Carias et al.(1976). They compared distances derived from 6 dental traits to the geographical and genetic distances between 7 Yanomama villages. They found a significant correlation between dental and geographic (Spearman's rho = .492, $p < .05$) and genetic (rho = .597 $p < .01$) distances.

2.5. Non-genetic factors influencing cranial morphology.

The preceding sections have presented the evidence for the genetic basis of cranial morphology. This section will briefly review other specific factors which may affect the form of adult crania.

2.5.1. Age.

In most morphological studies, it has been customary to regard data on all individuals over some arbitrary age (usually 18 years) as comparable (Lasker 1953). There is evidence, however, that this assumption is unwarranted, both for metric (Lasker 1953, Baer 1956, Garn et al. 1967, Israel 1973, 1977, Ruff 1980) and non-metric (Ossenberg 1970, Corruccini 1974, Berry 1975, Korey 1980) traits.

Metric traits.

Lasker (1953) studied over 600 living Mexicans from 19 years to over 51, and found that in males, head height, head breadth and zygomatic breadth increased in direct proportion to age. Facial height increased in females but decreased in males, probably secondary to alveolar resorption following tooth loss. Baer (1956) examined over 5,600 white male U.S. Army recruits, and found that total facial height, nasal height and bizygomatic breadth showed significant increase during the third decade of life. Head length and breadth, however, did not change.

Garn et al. (1967), studying both sexes in several racial groups, found that growth in skull length continued into the eighth decade. In a longitudinal study they found that skull length increased by 3% between 15 and 24 years. Israel (1973, 1977) found that the craniofacial system grows throughout adulthood, both cranial thickness and length increasing up to the eighth decade. Ruff's (1980) study of a skeletal series of American Indians confirmed Israel's findings that craniofacial growth continues throughout adulthood. He warned that comparisons between populations of different demographic structure might result in observed differences that are due to age characteristics alone rather than genetic or environmental distinctions.

Non-metric traits.

Berry and Berry (1967) claim that one of the many advantages of non-metric traits over metric ones is that they do not vary with age. Others have questioned this claim. Ossenberg (1970) described a pattern of association between age and expression, which varied with the type of trait. Hypostotic traits (those representing a relative insufficiency of osseous development, e.g. metopism, foramen of Hüshke) tend to decrease in frequency up to a certain age, after which they remain stable. Hyperostotic traits (those characterised by an excess of ossification, e.g. pterygo-basal bridge, palatine torus) tend to increase in frequency with age. Ossenberg interprets these tendencies to mean that these traits "achieve expression at variable times during post-natal development". She nevertheless concludes that the small frequency differences associated with age should not greatly alter the significance of genetic distance studies.

Finnegan (1978) studied age dependency in infra-cranial discrete traits, looking at young and old groupings within each sex, side and race. Significant differences (Chi-square test) in trait frequency of old and young subgroups did not exceed the number expected due to chance alone. Corruccini (1974), however, observed twice as many age associations as expected by chance within each sex and race subgroup. Unlike Finnegan, however, he did not separate the sides; this provoked criticism from Perizonius (1979b), whose own study of age dependence in cranial traits revealed only the number of associations expected by chance. Perizonius (1979a) points out that frequency tables based on the number of sides assume that left and right sides are independent. Surprisingly, he advocates halving the numbers in the table, seemingly unaware that this procedure carries the counter-assumption that the sides are perfectly correlated.

Berry (1975) tested age dependence of traits by dividing the sample into two subgroups on the basis of trait presence or absence, and testing (t-test) whether the mean age of the subgroups was significantly different. For only one of 22 testable traits was a significant value found, while two more had values approaching significance. She concluded that "age correlations need not be considered when dealing with adult material". Carpenter (1976), however, after comparing the discriminatory value of metric and non-

metric traits, concluded that "although the non-metric variables are better predictors of age than the metric variables, they are not particularly strong indicators". A further example of age dependence in non-metric traits was provided by Korey (1980). He partitioned a sample of 124 crania into 4 age categories, and demonstrated that the proportion of individuals manifesting the trait 'supra-orbital foramen complete' increased with age.

In any study of population affinity, therefore, it is desirable that the age distribution of the groups is similar. Ideally, the average age of each group should be determined, though in practice there are wide margins of error in the ages assigned to individual remains. In the present analysis, although mean ages are not available, it seems reasonable to suppose that the age profiles are more or less homogeneous between races and sexes.

2.5.2. Sex.

Metric traits.

Sexual dimorphism has long been recognised as an important factor affecting measurements, and metric studies have traditionally separated the sexes. Some workers, in an attempt to retain reasonable sample sizes, have pooled the sexes (Musgrave and Evans 1980, Van Gerven et al. 1977, Carlson 1976), but where sample sizes permit, separation of the sexes is desirable. The difficulty of accurately determining sex in human skeletons is another complicating factor.

Non-metric traits.

Berry and Berry (1967) claimed that trait expression is independent of sex. They tested this hypothesis by combining all the groups in their study to produce grand male and female samples, and calculating the MMD between them. Since the result was not significant, they concluded that sex differences were absent. This pooling of samples is criticised by Corruccini (1974) since sex variation over different samples could be cancelled out by summing groups with different combined frequencies. Corruccini found significant sex differences in 19 out of 61 traits for U.S. Whites, and 9 for U.S. Negroes (3 only would be

expected by chance), though the pattern of sex differences varied. He recommended that the sexes be studied separately, as in metric studies.

Berry's (1975) investigation of sex association revealed significant values in 7 out of 29 traits (1 to 2 expected by chance). She compared her sample with three other populations, and concluded that although sexual differences do occur, there is little consistency in their occurrence in different populations, and a variant more common in males of one sample may predominate in females of another. She recommends that studies should include equal numbers of the sexes where possible, but considers that sex differences "may well dilute each other or act in opposite directions in different samples", so that the distinction between populations may be unaffected.

Finnegan and Marcsik (1979) studied 6 populations (left and right sides examined separately) and noted the occurrence, in at least one group or side, of a significant sex association in 25 out of 42 traits. In each group on each side, the number occurring exceeded chance expectation, but the pattern of occurrence was inconsistent. Perizonius (1979b) found sex difference to be significant in 7 out of 45 traits (16%); he also recalculated Corruccini's (1974) results, using the previously mentioned method of halving the counts in the table, and found that the proportion of significant values fell to 8%, as opposed to Corruccini's value of 31%. Perizonius recommended that those few traits which showed a sex difference should be excluded from any analysis. Finnegan and Marcsik (1979), rejected this method since the large number of sex-varying traits found in their study (59.5%) would severely limit the number of traits available.

Cosseddu, Floris and Vona (1979) also studied sex difference in traits, using a variety of statistics. Using the chi- square test they found 4 significant values out of 32 tests (12.5%), but the proportion fell to 6.25% when they used the Grewal-Smith transformation on each trait. They concluded that, in general, sex differences were of little importance.

2.5.3. Chewing stresses.

Metric traits.

It is known that the action of muscles can influence the skeletal structure, as shown by bony crests and flaring gonions (Scott 1957). Palate dimensions have been shown to relate closely with diet type, being larger in populations with hard diets (Hunt 1959, McCann et al. 1966). Experimental work on rats (Watt and Williams 1951, Moore 1965, Beecher and Corruccini 1981a), macaques (Beecher and Corruccini 1981b) and squirrel monkeys (Corruccini and Beecher 1982) has demonstrated that animals fed on a soft diet do not attain the same facial breadth as control animals.

Weijs and Hillen (1986) studied the correlation in man between the cross-sectional area of the jaw muscles, and craniofacial size and shape, and again noted that hard diets could influence zygomatic breadth Corruccini et al. (1985) noted a decrease in facial height and increase in facial width in Kentucky whites "raised on unprocessed staples". Wolpoff (1968) suggested that the nasal and subnasal areas may also be affected by masticatory stresses.

Non-metric traits.

Chewing stresses, which have been shown to influence craniofacial dimensions, might well be expected to affect the expression of some non-metric traits, since many traits achieve full expression only after puberty (Buikstra 1972, Ossenberg 1970). Few studies have addressed this problem, except in the case of oral tori. Thoma (1937) identified 4 types of palatine torus, and stated that some types are due to masticatory buttressing while others are genetic. Many workers have noted the prevalence of oral tori in populations undergoing masticatory stress (Johnson 1959, Hrdlicka 1940, Matthews 1933, Hooton 1918). Mayhall and Mayhall (1971) also state that diet may affect the incidence of mandibular torus.

In the present study, the effects of diet are not considered since it seems likely that all the groups were of a similar subsistence level.

2.5.4. Cranial deformation.

Metric traits.

Cranial deformation, whether caused by cultural practices such as head binding, or post-mortem by earth pressure, has a marked effect on measurements, especially of the vault. Deformed crania were excluded from the metric study, except where sample sizes were very small, in which case measurements were taken only from areas such as the face, which seemed to have escaped deformation. No cases of cultural deformation were encountered in the samples employed.

Non-metric traits.

Post-mortem distortion does not affect non-metric traits; cultural deformation, however, has been shown to affect the incidence of wormian bones. Ossenberg (1970) showed that deformed crania had a higher incidence of posterior wormians, where growth was restricted by the cradle-board, and a lower incidence of lateral wormians where "the skull was free to expand to meet the growth demands of the brain". Emissary foramina were also more frequently present in deformed skulls. In males, facial sutures (os japonicum trace and infraorbital suture) were found less often in deformed skulls. The frontal region of deformed skulls also showed an overall significant hypostotic effect, as shown by the lower incidence of supraorbital and supra-trochlear foramina, frontal grooves, and trochlear spur and a slightly lower incidence of metopism. Regarding variants of the cranial base and mandible, 10 out of 11 traits showed an apparent hypostotic effect.

Other workers have also reported an increase in the incidence of wormian bones in deformed crania. Dorsey (1897) found that 10 out of 35 deformed adult Kwakiutl skulls had one or more coronal ossicles. He concluded that:

> artificial pressure on the head of the child has a tendency to lead to anomalous conditions in the suture which is most intimately affected.

Finkel (1971), studying crania from Lachish, found a correlation between the presence of wormian bones and the morphological and metrical observations indicative of "environmental stress".

2.5.5. Disease.

Metric traits.

Various pathological states can influence skull morphology. Brothwell (1981) summarises the abnormalities that may be encountered. Any abnormality of growth pattern is of major concern in craniometric studies, and any skulls showing gross pathology should be discarded. Nutritional status may also affect measurements; Pucciarelli (1980, 1981) has shown in rats that malnourishment or undernourishment during the growth period has a profound effect on the final shape of the skull. Stini (1969) suggested that in man, sexual dimorphism decreases under nutritional stress, which may influence skull size in the males of some populations. Angel (1982) has shown that cranial base height (porion-basion) is positively correlated with good nutrition, so that measurements which employ basion may be less justifiable when nutritional status is not known.

Alveolar resorption, secondary to tooth loss is another pathological factor which affects measurements, especially those relating to the point 'prosthion', and palatal measurements. Edentulous specimens show marked remodelling of the maxillary region, and should ideally be discarded where sample size permits; otherwise it may be possible to estimate the original position of prosthion. A subjective assessment of the dental health of the series used in this study marked only one group (Pieria) where the dental health was significantly worse than all the others.

In this series, some of the crania from Greece exhibited a spongy thickening of the vault bones (porotic hyperostosis), a condition often associated with hereditary anaemias. This was most marked in crania from Sindos, and Angel (1971) also reported similar cases in crania from Lerna. Both of these sites were situated near marshes, and the higher incidence of hyperostosis may reflect a higher population incidence of thalassaemias, as an adaptive response to malaria. Grossly thickened specimens were excluded from the study.

Non-metric traits.

Few studies have concentrated on the effects of health parameters on non-metric traits. The remodelling associated with tooth loss may affect some localised traits; Dunbar et al.

(1968, cited by Axelsson and Hedegaard 1985) showed that in Icelandic skeletal remains, torus palatinus was significantly less common in edentulous crania. Aural exostoses may sometimes be caused by disease (Roche 1964). Bennet (1965) notes that head stress, as seen in hydrocephaly, results in an increased number of wormian bones, while Hess (1945, 1946) relates wormian bones to metabolic disorders of the mesoderm. Orbital osteoporosis has been shown to be affected, if not caused, by hereditary and iron deficiency anaemias (Hengen 1971, Cybulski 1977).

2.5.6. Climate.

Metric traits.

There is evidence that the shape of the human cranium shows correlations with climatic environment. Beals (1972) studied cranial index in populations from four zones of climatic stress, namely, dry-heat, wet-heat, dry-cold and wet-cold. His results showed a clear gradation from the lowest values in dry-heat zones, through wet-heat and wet-cold to the highest values in dry-cold climates. Guglielmino-Matessi et al. (1979) discovered high correlations between Howells' (1973) global population data and several climatic indicators. Wolpoff (1968) similarly demonstrated that skeletal nasal aperture showed a range of variation between hot-wet and cold-dry climates.

Using a regression technique to eliminate climatic effects, Guglielmino-Matessi et al. were able to resolve to a great extent the discrepancy (Howells 1976) between the anthropometric and genetic picture of racial origins. In the present work, however, all the specimens come from a hot-dry climate and so no attempt is made to alter the morphological distances to take account of climate.

Non-metric traits.

To the author's knowledge, no studies have been undertaken which attempt to relate non-metric traits to climatic conditions. However, many workers have reported a correlation between metric and non-metric traits (Cheverud, Buikstra and Twitchell 1979, Corruccini 1976, Bennet 1965), so that it is not impossible that the climatic factors which influence growth patterns may affect non-metric, as well as metric traits.

3

THE CONSTRUCTION AND INTERPRETATION OF MORPHOLOGICAL DISTANCES.

3.1. Introduction.

The construction and evaluation of distances between populations involves four stages:

1. The representation of anatomical structure by numbers,
2. The utilisation of these numbers to produce a single measure of distance between two groups,
3. The production of a measure of statistical significance of the distances obtained, and
4. The examination of the matrix of distances to evaluate population affinities.

A general discussion of these four stages follows, after which their implications for metric and non-metric traits will be outlined. Special emphasis is placed on sources of error which may affect the distances obtained, and their interpretation.

3.1.1. The numerical representation of morphology.

The first step in the construction of population distance measures is the representation of anatomical structure by numbers. In order to have confidence in the accuracy of the distances obtained, the numerical values on which they are based must adequately represent the salient morphological features of the crania in the groups. Four questions relating to this topic will be considered:

1. What factors influence the choice and number of traits used ?
2. How adequately do the measurements and scores utilized reflect morphology ?
3. How reproducible are the measurements and scores ?
4. What problems are raised by lateral asymmetry in the crania ?

3.1.2. The production of a single measure of distance.

This involves the use of a formula which condenses the information in the data into a single value. For metric traits, this is the Mahalanobis distance and for non-metric traits the Mean Measure of Divergence. Errors in these distances may arise from two sources:

1. The formulae require that certain assumptions about the nature of the data must be made, violation of which can result in error. An account of these assumptions, and of the statistics used to test the data for these assumptions will be given.

2. Small sample sizes may also give rise to errors. These errors will be discussed, and some suggestions made whereby maximum information can be extracted from small and fragmentary samples.

3.1.3. Tests of significance.

Having obtained a matrix of the distances between all the groups considered, the statistical significance of these values can aid in the interpretation of the results. Significance levels, however, may not always be accurate, and may lead to confusion rather than clarity when evaluating population affinity. Too much emphasis on formal tests of significance is therefore not advised.

3.1.4. Evaluation of population affinities.

The distance matrix represents a simplification of the information in the raw data but may, nevertheless, be difficult to interpret by visual inspection. Plotting the groups in two or three dimensions, so that the distances between the points are preserved as much as possible, greatly facilitates interpretation. The methods employed to achieve these plots will be outlined, and the superiority of plots over significance tests will be discussed.

3.2. Metric traits.

3.2.1. The numerical representation of morphology.

3.2.1.1. Choice and number of measurements.

Skull measurements attempt to characterise the shape and size of the cranium and much discussion stems from considerations of the number and types of measurement that need to be

taken (Oxnard 1984). Certain shapes may be characterised by a few measurements. A single measurement for a circle or sphere supplies full information while two define a rectangle and three a box. Biological examples are, of course, much more complicated and more measurements are required. In some cases, absurdly large numbers have been proposed and recorded. Howells (1969b) mentions a study in which over 5000 measurements were suggested as being necessary to describe a human skull.

Though a few measurements may not adequately define shape, very large numbers, beyond a certain optimum point, may add very little true information but a great deal of noise. Oxnard (1984) showed that for the primate scapula, nine measurements gave as much information as seventeen and for the talus, sixteen measurements produced results that did not differ from the results derived from eight. The shape of the cranium is much more complex and Howells (1973) considered that it may not be adequately described metrically until fifty-seven measurements have been taken.

In this work, however, discrimination between groups is required rather than a full representation of cranial shape and many workers (Musgrave and Evans 1980, Rightmire 1976 among others) have adequately discriminated between groups using fewer variables. Statistical considerations also enter the argument. If the data matrix contains too many highly correlated variables it may not be of full rank (i.e. it may contain redundant information in one or more rows or columns). Under these circumstances, numerical problems can arise if there is too much redundancy; interpretation of the results also becomes difficult. (Conversely, if the variables are uncorrelated, multivariate methods are inappropriate since the reduction in dimensions which they achieve depends on deriving uncorrelated linear combinations from weighted correlated variables).

A further consideration is that large numbers of variables lead to the necessity for larger sample sizes. Kendall (1975) recommended an overall sample size of at least 10 times the number of variables. Van Vark (1976) and McHenry and Corruccini (1975), discussing discriminant function analysis, maintain that the sample size of the individual groups should also be considered. They suggest that to avoid the introduction of statistical

artefacts, the number of variables should be less than the number of individuals in the smallest group.

With regard to the choice of measurements, Keita's (1983) criterion of adequate coverage of morphology and maximum genetic basis should be borne in mind, as well as statistical considerations regarding degree of trait correlation. A further factor in this study stems from the use of groups measured by other workers who followed the Biometric Laboratory school of measurement, whereas the author used those formulated by Howells (1973). Howells indicates those measurements which are synonymous with ones used in other systems; this reduces the choice of variables usable in the comparison of such groups to nine or ten. Since, however, Musgrave and Evans (1980) obtained similar results from the analysis of five, seven, eight and fourteen measurements, the small number of variables used in the present study is probably sufficient to discriminate between the groups.

3.2.1.2. The appropriateness of measurements in describing form.

The system of measurements employed in conventional craniometry has often been criticised (Yasui 1986, Hursh 1976, Moyers and Bookstein 1979) on the grounds that it is based, not on biological principles but on the "constraints of tradition and the instruments available " (Yasui 1986). The majority of measurements record straight-line distances between defined points. Moyers and Bookstein (1979) state that a sound measure of form must take into account the curving of the form being measured, and they criticise conventional measurements on the grounds that:

> . . . (the) straight line along which the distance is measured has no biologic (sic) reality, for it describes neither direction of growth, lines of stress, directions of muscle pull, nor the lineaments of form in between.

As well as lacking 'biological meaning', linear measurements also fail to adequately represent three-dimensional geometry since they record only magnitude and not orientation.

Dissatisfaction with this reduction of form to dimension-free magnitude has led to many attempts to develop methods which more rigorously define form and change in form in geometric terms. Sneath (1967) adapted geological trend surface analysis to biological forms. Blum (1973) devised a method called symmetric axis analysis where the shape of an

outline can be collapsed into a curve drawn through the centres of a set of circles which touch the boundary of the bone at two distinct points. Lestrel (1974) used Fourier analysis and its derived harmonic amplitudes to represent complex forms in a comparison of hominoid skeletons. Bookstein (1978) devised the biorthogonal grid as a method of representing change in form by measuring stretch along the principal axes of the deformation of one form to another. The shape of such grids is defined by the form change itself, unlike the standard rectangular grid devised by Thompson (1961), and measurements taken include both the magnitude and direction of maximum stretch.

Although these methods have been successfully applied in many fields (e.g. orthodontic cephalometry and allometry studies), their use in anthropology has been limited. This is because these geometrical representations do not readily lend themselves to the quantitative study of population-level variation:

> Since most theories of functional and evolutionary morphology are statistical in nature, it is difficult to interpret the results of the geometric methods in light of these theories. (Cheverud et al. 1983)

Two methods of reconciling a complex geometrical representation of form with statistical methods of analysing variation have recently emerged. Yasui (1986) presented a method of analysing outline where an average outline could be generated statistically and intra- and inter-group variation assessed. He applied the technique to the analysis of sexual differences in the midsagittal outline of recent Japanese crania and demonstrated subtle features which could not be detected by traditional measurements. Cheverud et al. (1983) proposed a method using three-dimensional coordinate point definitions of landmarks. They employed finite element analysis to produce an average form for, and analyse variation in, a series of male rhesus macaque skulls. Both of these methods include an analysis of allometry (i.e. size-related shape change), though Yasui discerned no evidence of allometric change in human crania of either sex.

Although more sophisticated methods of describing cranial shape are now available, traditional methods should not be discarded. Distances derived from metric variables should reflect differences in the population gene pools (Hiernaux 1972). Measurements such as skull length may contain a component of neural as well as osseous growth (Baer and

Harris 1969), but, provided that the same portion of the genome is represented by the measurement in different populations, the actual function of the genes is immaterial. Many heritability studies based on traditional measurements have indicated that their variation contains a significant genetic component. Family studies which use these new methods have yet to be undertaken and, until evidence emerges that alternative measurements are significantly more heritable than traditional ones, or less susceptible to environmental fluctuations, traditional metrics are still of value in determining population distances.

3.2.1.3. Reproducibility of measurements.

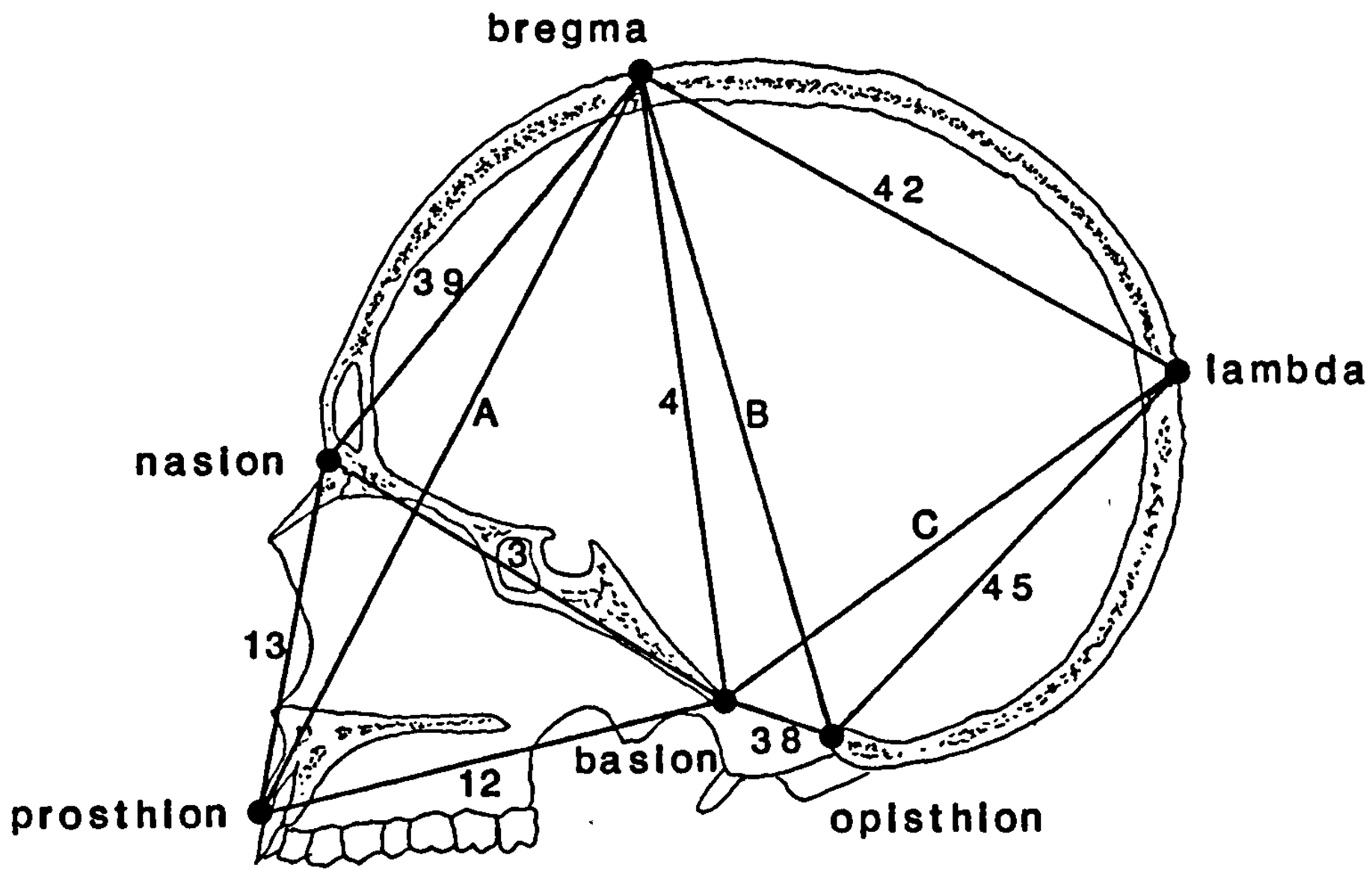
Mahalanobis distances are based on differences in the sample means of the measurements. The accuracy of the mean values depends, not only on statistical considerations such as sample size, but also on the degree to which measurement error can distort the values. Jamison and Zegura (1974) and Utermohle and Zegura (1982) found disturbingly high levels of inter- and intra-observer error in their analyses of Eskimo craniometric data.

Measurement error is to some extent unavoidable since measurements are rounded to the nearest millimetre. There is a tendency to round up measurements falling midway between two values, which tends to overestimate the mean. (An improvement on this practise would to be round such readings up and down alternately). The position of landmarks may also vary, according to the convenience of caliper placement, an example being prosthion which may vary from the front to the underside of the alveolar margin with basal and facial measurements (Hursh 1976). That many calipers have rounded ends is a further factor which makes accurate landmark placement difficult.

One procedure which may help to reduce measurement error is the adoption of the 'truss' system of body form reconstruction, as advocated by Strauss and Bookstein (1982). Traditional craniometric distances usually employ triangulation, measuring the distances between three points (e.g. between basion, nasion and prosthion). Strauss and Bookstein point out that the adoption of a quadrilateral system allows recording of the two diagonals as well as the four sides between four points (see fig. 3.1). The two diagonals act as checks

Fig. 3.1 Patterns of distances among 10 coplanar landmarks.

Fig. 3.2 The truss method applied to the human cranium.



Standard measurements (Howells 1973).

3. Basion-nasion length.
4. Basion-bregma height.
12. Basion-prosthion length.
13. Nasion-prosthion height.
38. Foramen magnum length.
39. Nasion-bregma chord.
42. Bregma-lambda chord.
45. Lambda-opisthion chord.

New measurements required for truss.

A. Prosthion-bregma.
B. Opisthion-bregma.
C. Basion-lambda.

on the side measurements. When the landmarks are plotted according to the measured distances, errors in the readings result in the points occupying more than two dimensions. Mathematical methods can be used to flatten the truss which "preserve . . . the sum of the lengths in the truss cell, while balancing error-of-fit about all six measurements."

Strauss and Bookstein illustrate their paper with midsagittal outlines of fish. The globular shape of the human cranium, and the fact that the four points must lie in the same plane, makes adoption of the truss system more difficult, but fig. 3.2 suggests how it could be applied to midsagittal measurements of the cranium, and lists the new measurements which would need to be taken between the familiar landmarks.

Apart from measurement error, Utermohle, Zegura and Heathcote (1983) present clear evidence that certain craniometric dimensions expand with increasing levels of relative humidity, especially in crania which have not been treated with polyvinyl acetate. One treated and one untreated skull were measured at relative humidities of 18% and 98%. Of the 40 variables recorded, 8 (including nasal and orbital heights) were invariant. Of the remaining 32 variables (average value 99mm. at 18% r.h.), in the treated skull, 18 showed an average increase of 1.1mm., while in the untreated skull, 31 variables increased by an average of 1.5mm. This experiment emphasises the advantages of treatment with polyvinyl acetate where crania are to be used in metric analysis.

Utermohle, Zegura and Heathcote conclude:

> The ubiquitous nature of significant measurement imprecision should be a cause of concern among craniometrists. The potential inappropriateness of conclusions involving data collected by different observers is not a comforting prospect for a scientific discipline.

The impact of measurement errors on the computation of population affinities is difficult to gauge, but if the differences between individual population means are of the same order as differences attributable to measurement error then the conclusions must be viewed with circumspection.

3.2.1.4. The problems of asymmetry.

Left-right asymmetry is rarely a problem in metric analysis. Most measurements are taken in the midline, or cross the midline so that the left and right halves of the skull are

encompassed. In some cases, however, such as the orbital measurements, a decision must be taken whether to use only one side, or both sides as separate traits, or to take the average of the two sides as a single variable.

This decision is somewhat arbitrary, though if both sides are highly correlated, there is little information gained by using both left and right measurements as separate traits. Howells (1973) uses the left side of the skull for measurements where a choice must be made, with the exception of mastoid measurements where the average of both sides is taken. Where the crania are damaged, however, he recommends that the series of measurements (such as the projections from the transmeatal axis) be taken on the right since:

> It is more important to preserve the relative degrees of projection of each point among the set on one side than to get the left measurement where it is available.

The orbital height and width are similarly treated, taking both measurements on the right as "the best means of estimating the diameters of the left orbit" if the left is damaged. Howells' method is the one adopted in this work.

An alternative approach may be of value if the proposed method of data analysis can utilise incomplete crania. If such an approach is used (see 3.2.2.2.) it is important to have the best possible estimate of the mean. Rao (1952, p.161) gives a formula for finding the best estimate of the means of two highly correlated measurements where information on one or other variables is missing for part of the sample. If this method is followed, provided the sample is fairly large, right and left values should be recorded, and all the information used to get the maximum likelihood estimate for the mean of the left side.

3.2.2. The Mahalanobis distance: sources of error.

The distance measure employed with metric variables is the Mahalanobis distance (D). This is a Pythagorean distance which standardises the variances of the variables, and takes account of correlation between the measurements. The formula for the squared distance, in matrix notation, is

$$D^2 = (\bar{x}_i - \bar{x}_j)' S^{-1} (\bar{x}_i - \bar{x}_j),$$

where $\bar{x}_i$ and $\bar{x}_j$ are vectors of length p (p = number of measurements) containing the means for groups i and j respectively, and S is the pooled within-group dispersion (or variance-covariance) matrix for all the groups. Essentially, D^2 is a straightforward summation, for all measurements, of the squared differences between the group means, and D is therefore a Euclidian distance. The inclusion in the formula of S^{-1}, the inverse of the variance-covariance matrix, has the effect of transforming the individual measurements into standardised, uncorrelated variables. For a full account of the derivation of this formula, consult Mardia, Kent and Bibby (1979 pp.14-17).

Errors in the Mahalanobis distance may arise from two sources. Firstly, the mathematical assumptions on which the distance measure is founded may be violated by the data. Secondly, small sample sizes, and different numbers of observations for each trait, may have an effect on the distances. These two sources of error will now be discussed.

3.2.2.1. The violation of mathematical assumptions.

The formulation of the mathematical expression for the Mahalanobis distance involves the multivariate extension of univariate statistical theory. Hence, assumptions are made about the qualities and distributions of the data, (viz., that the data come from a population with a multivariate normal distribution) which should be confirmed if the use of these methods is to be justified.

Calculation of the distances involves the pooling of the individual group dispersion matrices to give an overall measure of within-group dispersion. Implicit here is the assumption that the individual matrices are homogeneous i.e. that the correlations and variances of the measurements are the same in all groups. It is desirable that this assumption be tested, though there is a body of empirical evidence suggesting that multivariate methods are fairly robust to departures from homogeneity (Blackith and Reyment 1971). Furthermore, tests of homogeneity are formulated on the assumption that the data examined have a multivariate normal distribution, and they are sensitive to departures from this distribution.

A second source of error in the distance arises when the groups have different sizes. Rao (1952 p364) gives a formula for the correction for bias of the D^2 values when sample sizes differ, and different numbers of observations occur for each measurement. He notes, however, that:

> The effect of sample size in the estimate of D^2 is not very serious and can easily be corrected if necessary, . . . by subtracting some value which depends solely on the sample sizes and whose value is negligible (tending to zero) in large samples. Comparability is retained because the weights attached to the various characters are not functions of sample sizes.

Rao's correction was not used in the present study, since it tends to render the final distances non-Euclidian, and if the sample sizes are fairly large "the correction is trivial and need not be carried out" (Rao 1952). Also, very small D^2 values may sometimes be rendered negative by this correction.

3.2.2.2. The effect of small sample size and incomplete data.

The question of appropriate numbers for a sample has long been a problem (Broca 1875, Olivier et al. 1965, both cited by Howells 1973), though Howells (1973) decided on 50 or more of each sex as being appropriate for his study. Anthropologists studying ancient human remains are often frustrated by the small size and fragmentary nature of the samples with which they have to work. Sample sizes of 10 or fewer crania are not uncommon in the literature (Rothhammer et al. 1982, 1984, Musgrave and Evans 1980, Zegura 1975).

The sexual dimorphism apparent in metric traits requires separation of the sexes, which further exacerbates the problem of sample size, as well as introducing another source of error from incorrect sexing. Howells (1973) notes that "all expressed opinions doubt that more than 90 percent of skulls can be correctly sexed by eye", and sexing by discriminant function analysis has little more success (Giles and Elliot 1963). Furthermore, Weiss (1972) detects an additional systematic bias towards males of 12% throughout several skeletal studies.

Some workers (for example, Musgrave and Evans 1980, Carlson 1976, Van Gerven et al. 1977) have combined the sexes in an attempt to maintain acceptable sample sizes. This expedient has been criticised (Hillson 1978 p. 90), but may be justifiable where there are

equal numbers of males and females in each sample. Combining unequal numbers of the sexes affects the Mahalanobis distance in two ways: the group dispersion matrices are likely to be heterogeneous, and the differences in the means will reflect sexual dimorphism as well as population distance. Despite these reservations, this method has produced plausible results (Musgrave and Evans 1980).

Where sample sizes are small, the interpretation of the Mahalanobis distances is problematical. The variance of small samples is usually underestimated, though the correction of dividing the sum of squares by the degrees of freedom rather than the sample size generally compensates for this. Also, the pooling of the dispersion matrices tends to iron out any discrepancies, provided that the pooled matrix has a sufficiently large value for the degrees of freedom. Tests of homogeneity of the pooled dispersion matrix may also highlight groups where the variance estimate is atypical.

The major source of error lies in the estimation of the means, since it is the difference in the group means which form the basis of the Mahalanobis distance. Examination of the 95% confidence interval for the means, and its comparison with the differences between the group means may aid in assessing whether the Mahalanobis distance is a reliable indicator of distance. This could be a cumbersome process were it not for the fact that all the variables do not contribute equally to the distance. By breaking down the distance into its component parts, the transformed variables, the most discriminating measurements can be found, and these ones alone need be checked.

The fragmentary nature of many samples is a further problem. Most computer packages containing programs for multivariate analysis are constrained to use only those units for which a complete set of values are present. It is a common experience in multivariate analysis that seemingly large samples contain a scarcity of values for certain measurements, which effectively reduces the sample size to that subset for which a complete set of variables is available.

One approach to overcoming this difficulty is the replacement of missing values with estimates. Essentially, the means, variances and correlations of all the variables from the complete subset of the group are used to predict a missing value from the individual's

remaining measurements. The GENSTAT program 'MULTMISS' (which uses a regression method similar to that of Orchard and Woodbury, 1972) is an example of a program which can be used to pre-process incomplete data. Use of such programs may be warranted where samples contain a large number of complete skulls, but the estimates are unreliable when more than 10% of the data is missing. This method may also be criticised on the theoretical ground that it assumes multivariate normality of the data.

In this work, a different approach to the problem of missing data is taken. The use of statistical packages is abandoned in favour of a 'custom built' program which calculates Mahalanobis distances using all the available data. This program, written in the GENSTAT language, is an adaptation of a program created by Dr. S. P. Evans of the Computer Centre, University of Bristol.

It has already been shown that errors in the means are of more importance than errors in the variances and covariances, since pooling of the dispersion matrices tends to smooth out discrepancies caused by small samples. The contribution of each group matrix to the pooled matrix is weighted according to the sample size. Hence, the inclusion of large samples in the analysis will compensate for errors in the variance of small samples, *provided* that the population dispersion matrices are believed to be homogeneous. In this case, the pooled matrix may be constructed from complete skulls, as long as the total number of degrees of freedom is sufficiently large.

All whole and incomplete crania are then used to derive the best (unbiased) possible estimate for the group means, and these values are entered in the formula for the Mahalanobis distance. This is the method used by Rao (1952), and his correction to the D^2 for differences in sample size may then be applied, if desired, as a simple addition to the program which calculates the D^2s.

Where several fragmentary samples are to be analysed, and the total number of complete skulls is small, the pooled dispersion matrix may be constructed using all possible values and pairs of values in the data. A sums of squares and products matrix (of differences from the group means) is constructed, a cell at a time, from all the data, and each cell of this matrix is divided by the degrees of freedom for that variable or pair of variables. The

best estimate of the group means are then found as before, but Rao's correction for sample size difference can not be applied in this case. This method should not be used if it can be avoided, but if samples consist mainly of incomplete crania, and no suitable large groups are available for comparison, it may be used to find the best possible estimate of the Mahalanobis distance.

3.2.3. Tests of significance.

Having obtained a matrix of Mahalanobis distances, their interpretation is aided by a knowledge of the significance of the distance values. With the commonly used group-based multivariate techniques, three types of significance test may be undertaken:

1. Tests of the homogeneity of the group dispersion matrices. These have already been mentioned in 3.2.2.1
2. Tests of significance of the distances between the groups. Groups which are not significantly different may, if desired, be pooled and treated as one unit (Rao, 1952).
3. Tests for the significance of the roots of determinantal equations. This last test indicates how many of the new variables have discriminating power.

Many statistical packages for multivariate analysis include significance tests (e.g. the GENSTAT program 'CVAID'), but interpretation of the results may not be straightforward. The reason for this is made clear by Chatfield and Collins (1980) in their description of multivariate data-analytical procedures:

> Like most procedures based on normal theory, they depend on the values of the sample means, variances and covariances, and so have a heuristic attraction independent of the distributional assumptions. Thus, it could be argued that these procedures are useful methods for the analysis of any data, although, of course, *significance levels are only valid when the distributional assumptions apply*. (my emphasis.)

Hence, although multivariate techniques may be used when the data is not multivariate normal, the associated significance tests will not be reliable.

Blackith and Reyment (1971) emphasise that there is as yet no definite method for testing multivariate normality. The variables may be examined separately for univariate normality; if the individual variables are not normal, then the multivariate distribution will not be normal. However, a set of univariate normally-distributed variables, when

considered together, is not necessarily multivariate normal. It is likely, though, that the multivariate equivalent of the central limit theorem of univariate statistics, (see Hoel 1984, p.132) is applicable, especially for biometric data, where many different factors (genes and environmental effects) contribute additively to the measurements.

Use of the methods proposed in 3.2.2.2 for dealing with incomplete data also presents difficulties for carrying out significance tests. Although formulae are available for testing the significance of the D^2 (Rao 1952), they can not be used when different numbers of individuals are used to determine the mean for each measurement. There is a trade-off here between obtaining the best possible estimate of the distance, and knowing if the distances are significant.

It has been argued that significance tests are not necessary for many multivariate studies (Blackith and Reyment 1971). Where reduced dimension plots of the data are examined visually to assess group affinities, the information in the plot may be of more value than a possibly dubious significance test. Blackith and Reyment also point out that knowing the result of a significance test is no substitute for a thorough knowledge of the data. With these comments in mind, the present work places little emphasis on obtaining significance levels for the distances obtained, but attempts, through a thorough examination of the data (using univariate and multivariate tests), to interpret their values in terms of population affinity.

3.2.4. Interpretation of the distance matrix.

The information contained in a distance matrix is often difficult to assimilate. For this reason graphical displays of the output from data are preferred. The various mathematical techniques collectively known as *multidimensional scaling* can be of great value in interpreting matrices of distances. These methods portray the different groups as points on a two- or three-dimensional graph in such a way that the distances between the points are the best possible representation, in that number of dimensions, of the Mahalanobis distances. The power of these scaling techniques has been frequently

illustrated by using them to reproduce the map of Britain from a matrix of road distances between towns (see for example, Chatfield and Collins 1980, Coxon 1982)

Two different types of multidimensional scaling may be recognised; these are *classical scaling* and *ordinal scaling*. In classical scaling (e.g. principal co-ordinates analysis (PCO)), the actual distances between the points are preserved as far as the dimensionality of the plot allows. In order to use classical scaling, the original distances must be Euclidian (i.e. obeying the laws of triangulation). Mahalanobis distances, if calculated from complete sets of data, and uncorrected for difference in sample size, are Euclidian distances, and may be plotted using PCO.

Ordinal scaling attempts only to preserve the rank order of the distances, and is appropriate where corrected D^2s, or ones derived from incomplete data are used. Chatfield and Collins (1980) note that, where distances are nearly Euclidian, ordinal scaling gives much the same result as classical scaling, and better results where non-Euclidian distances are plotted, and conclude that ordinal scaling is the better technique.

In this work, the distance matrices are examined using ordinal scaling (using the MDS(X) program MINISSA) since the various adjustments to the D^2 for sample size can be more easily justified if only the rank order of the Mahalanobis distances, rather than the values themselves, are considered. The significance of the distances between groups is kept in mind when looking at the plot, but no attempt is made to combine groups whose distances are non-significant, or to reduce their distance values to zero before plotting. The points are allowed to "speak for themselves" regarding their affinities; the credibility of their statements are left to the judgement of the observer.

3.3. Non-metric traits.

3.3.1. The numerical representation of morphology.

3.3.1.1. The choice and number of traits.

The number of cranial non-metric traits employed in various studies has ranged from 14 (Rothhammer et al. 1984) to 72 (Corruccini 1974). Most studies have used around 30 traits

(e.g. Berry and Berry 1967, 1972, Berry 1974, Kellock and Parsons 1970a, b, Ossenberg 1977, Finnegan and Marcsik 1979). Unlike metric variables, non-metric traits do not attempt to describe the overall morphology of the skull, but to reflect aspects of the gene pool. R. J. Berry (1979) referring to an earlier study on the house mouse (Berry and Jakobson 1975), states:

> The value of non-metric variants is that they provide an indication of the alleles carried by a large number of gene loci,... each variant might be the product of variation at 10 loci, so that 30 uncorrelated variants will involve the screening of 300 loci, representing a significant part of an average genome of about 10,000 loci.

Lewontin (1974), discussing electrophoretically detected loci, considered that at least 100 loci are needed to compare populations with any accuracy. Hence, if Berry's belief is accurate, at least 10 non-metric traits are necessary in a study where populations are compared.

The evidence that non-metric traits have a strong genetic basis stems mainly from the work of Grüneberg (1963) on inbred strains of laboratory mice. He noted, however, that prenatal and maternal influences (such as age, parity and lactational performance of the mother, and the size of the litter) could affect trait incidence. Howe and Parsons (1967) also demonstrated the effect of prenatal influences on individual trait incidences, but demonstrated that, if 20 or more variants were considered, the overall measure of genetic distance between strains remained virtually unchanged. A. C. Berry (1975), being unable to rule out the possibility of sexual dimorphism in non-metric traits also suggested that a large number of variants be used so that "sexual dimorphisms . . . dilute each other or act in opposite directions in different samples, so that . . . the final distinction between the samples is likely to be unaffected". These considerations indicate that "as many variants as possible which can be scored with reasonable objectivity as present or absent" (Berry and Berry 1967) should be used.

The limit to the number of traits used, which should probably not fall below 30, is to some extent arbitrary. A large number of variants should give a truer estimate of genetical difference between two populations, since a larger portion of the gene pools of the samples is compared (Berry and Berry 1972). However, traits may be excluded for several reasons.

Extremely rare traits may not be seen in some series, and Sjøvold (1973) warns that in this case, the trait should not be included in the mean measure of divergence. Traits which are strongly correlated with other traits should not be used, since the MMD assumes that traits are uncorrelated. Traits affected by sex should be excluded from studies where the sexes are pooled, and any showing a distinct association with age (excluding pre-adult stages) may cause errors if the age distribution of the samples are not equal.

3.3.1.2. The appropriateness of scores for describing form.

Although non-metric traits are supposed to be judged by simple present-absent criteria, most traits in fact show a continuous range of variation. Corruccini (1974) notes that a number of workers have admitted occasional confusion in defining traits or drawing the line between present or absent. Sjøvold (1973) also notes that a trait may vary in appearance when present e.g. one or more accessory foramina or sutural ossicles may exist, but concludes that "the essential question is whether the variant is present and not how it is present".

This assertion could be criticised on the grounds that different degrees of trait expression may represent different genetic influences. Anderson (1968, cited by Corruccini 1974) showed that tubercle development may be poor in some populations, though present-absent variation exists. As well as possibly reflecting different genes, this variation in degree of development might cause different observers to have different threshold locations; similarly an observer might change his threshold value when confronted with a group exhibiting well developed tubercles.

Corruccini (1974) therefore recommends an ordinal scoring system based on the grade of development of the trait. This method also allows for the recording of partial manifestations of traits, which some workers (Cheverud and Buikstra 1978, Buikstra 1972) regard as synonymous with full trait expression. Unfortunately, ordinal scores cannot be used with the Grewal-Smith MMD (though some of the 'genetic distance' measures (see section 1.3.2) have no such limitation), so that they must be converted to binary scores by deciding on an appropriate threshold value. Ordinal scoring can, however, be useful in preliminary analysis of the data, and partly overcomes the problem of 'drifting

thresholds'. Although as much difficulty obtains in deciding between, say 'trace' and 'intermediate' scores in an ordinal scale as between present and absent in the binary model, a more detailed description of variability is attempted.

3.3.1.3. Reproducibility of the scores.

One of the major advantages non-metric traits are purported to possess is the ease with which they can be scored and standardised (Berry and Berry 1967). Molto (1979), noting that this view has been challenged, studied intra-worker error in the scoring of discontinuous traits . Utilising the Phi coefficient for dichotomous data, he found that the degree of error varied with the method of scoring. When only the full expression of the trait was scored as present, most of the 50 traits he examined had a very high scoring consistency, with the following exceptions:

Mastoid foramen absent
Accessory lesser palatine foramina
Anterior ethmoid foramen exsutural
Accessory infraorbital foramen
Pharyngeal fossa
Foramen of Vesalius
Accessory foramen spinosum

When partial manifestations of the trait were included in the definition of 'present', as recommended by Buikstra (1972), scoring consistency was somewhat lower, especially where the incidence of the complete trait was low.

Molto also compared the MMD for four groups using two sets of traits, one including, and one excluding the traits with poor reproducibility. The smaller set of traits was found to reflect more accurately the relationship between the groups. Molto recommends that workers check their data for scoring error, and discard those traits with poor reproducibility.

3.3.1.4. The problem of asymmetry.

The M.M.D. is calculated from two quantities:

p - the trait incidence or frequency, and

n - the sample size or number of observations.

For midline traits the determination of *p* and *n* is straightforward. Bilateral traits, however, present a problem since an asymmetric expression of the trait is frequently encountered (Trinkhaus 1978, Perizonius 1979a). Unfortunately, at present there is no standardised method of deriving frequencies for bilateral traits and as Perizonius (1979a) points out:

> Even the most sophisticated statistics give wrong results if based on incorrect p's . . . and n's . . . For this reason, the crucial problem of how to evaluate median and lateral non-metric traits requires attention.

Different authors have used a variety of procedures in calculating ps and ns. These are now outlined:

1. Berry and Berry (1967) in their original publication based their *p*s and *n*s for lateral traits on the number of sides, in contrast to the median traits where they are based on the number of individuals. In doing so their sample sizes for lateral traits were twice those for midline ones. This method assumes that both sides are statistically independent.

2. Kellock and Parsons (1970a, b), Sjøvold (1973) and Perizonius (1979a) suggested that, since most traits show a strong preference for symmetry, *p* should be based on sides and *n* on half the number of sides. This method assumes that both sides of the skull are perfectly correlated.

3. Green, Suchey and Gokhale (1979) devised a method where *p* is based on the number of sides. When the left and right frequencies are the same, this method will produce an unbiased estimate of *p* even when incomplete material is included. If the left and right frequencies differ, then *p* is an estimate of the average for the two sides (provided only complete skulls are examined).

   The sample size, *n*, is based on the number of sides with a correction factor based on the left-right correlation coefficient. With this method, imperfectly preserved crania can also be utilised. Let

   m = the number of intact crania where the trait is detectable on both sides,

   mr = the number of crania with only the right side intact,

   ml = the number of crania with only the left side intact,

then,

$$n = \frac{N^2}{N + 2m\rho} ,$$

where the total number of sides examined, N = 2m+mr+ml, and ρ is the correlation of trait occurrence from side to side. In practice, ρ, the population correlation coefficient is unknown, but *r*, the sample estimate of ρ, can be used. Although this introduces sampling errors, Green, Suchey and Gokhale claim that the error is "of lower order of magnitude than the error introduced by ignoring the side to side dependence."

This coefficient *r* is calculated, for each group in turn, from the two-by-two table shown below, using the following formula.

		Right side	
		Present	Absent
Left side	Present	a	b
	Absent	c	d

$$r = \left| \frac{(ad-bc)^2}{(a+b)(c+d)(a+c)(b+d)} \right|^2$$

4. Zegura (1975) calculated *p*s and *n*s using one side only for bilateral traits. This method makes no statistical assumptions, but if the material is badly preserved, then losing the information contained in the other side may be undesirable.
5. Korey (1980) suggested that *p* and *n* be based on the number of individuals by evaluating the asymmetric expression as identical to the symmetrical positive expression. Green, Suchey and Gokhale (1979) demonstrate that this method tends to produce lower values for *p* if imperfectly preserved material is used.

The preceding account of the different methods employed for calculating *p* and *n* evaluates them only from the statistical point of view. Korey (1980) asserts that biological principles, as well as statistical ones should be considered in the choice of sampling unit. The biological basis of asymmetry will now be discussed.

The biological basis of trait asymmetry.

Asymmetry of bilateral structures raises particular problems in relation to non-metric traits. Bilaterally symmetrical structures should in theory develop as mirror images. Mather (1953) proposed that fluctuating asymmetry (i.e. asymmetry without preference for one side) reflects interferences encountered in the attempt to render the same developmental message twice. These disturbing factors are non-genetic, though susceptibility to such interference depends on the genetic make-up of the individual. Mather, using fruit flies, found asymmetry to be increased with inbreeding. Bailit et al. (1970) found greater dental asymmetry in the Tristanites than in other less inbred groups, while Niswander and Chung (1965) demonstrated an association between degree of incisor asymmetry and consanguinity in Japanese children.

Environmental stresses have also been demonstrated to affect dental symmetry. Siegel and Doyle (1975), who subjected pregnant rats to audiogenic stress, found an increased asymmetry in their offsprings' mandibular molars. Bailit et al. (1970) have also shown that, in man, broadly defined environmental stress is positively related to dental asymmetry. Perzigian (1977) studied a prehistoric hunter population and found that the taller and ostensibly better nourished individuals had larger and less asymmetric teeth than the shorter ones. DiBennardo and Bailit (1978), conversely, found no association between prenatal stress and dental asymmetry in Japanese children. O'Rourke and Crawford (1977) also failed to demonstrate such effects.

An alternative explanation of the occurrence of bilateral asymmetry is the 'two-threshold theory'. Trait expression reflects the presence of a threshold on the curve of the normally distributed hypothetical 'underlying variate'; asymmetric occurrence is explained by the presence of two thresholds on the curve. Any individual whose underlying variate lies between the two thresholds exhibits the trait on one side only, and bilaterally if the second threshold is exceeded. This hypothesis has been favoured by Berry (1968), Czarnetzki (1971) and Ossenberg (1981).

Ossenberg (1981) presents evidence in favour of the two-threshold theory. She shows that, given the assumption that the distance between the two thresholds remains constant,

populations in which the trait is common (i.e. the underlying 'tendency' curve is shifted to the right) should show a greater proportion of bilateral occurrences than populations in which the trait is rare. Her examination of two traits in 27 population samples shows that there is an overall trend toward increasing bilateral occurrence with increasing incidence for both traits.

McGrath, Cheverud and Buikstra (1984), in an attempt to find supporting evidence for the two-threshold theory, studied the heritability of asymmetry in Rhesus macaque skeletons of known familial relationship. In only 2 out of 13 traits studied did they find heritability estimates significantly different from zero, from which they concluded that there is no support for Ossenberg's contention that asymmetry is genetically influenced.

The conflict between these two theories is not just a matter of academic interest; which one is believed has a fundamental effect on the way that traits are scored. The two-threshold theory asserts that:

> ...phenotypes with more pronounced expression (bilateral occurrence) have greater genetic potential than those with less pronounced expression (unilateral occurrence). Therefore, scoring traits in total left and right sides,by giving greater weight to bilaterally affected individuals, may provide a better estimate of the liability for the trait in the population.
>
> (Ossenberg 1981)

Korey (1980) confirms this:

> Sampling by side is consistent with the premise that trait expression on each side reflects an additive component of genetic variation.

Therefore, the scoring method of Green, Suchey and Gokhale (1979), which contains a statistical correction for side to side correlation, is the preferred method if asymmetries are thought to reflect additive genetic factors. McGrath, Cheverud and Buikstra (1984), however, criticise this method on the grounds that it applies to phenotypic correlation, and therefore "does not address the problem of whether sides provide redundant genetic information", and also that, in practice, it is difficult to use.

By contrast, the proposition that asymmetries result from developmental noise implies that sampling by individual is the correct procedure. The age regressive nature of many traits has been taken to indicate that unilateral expression represents a transient developmental stage (Korey 1980). Buikstra (Cheverud and Buikstra 1978, Buikstra 1972)

extends this line of reasoning to argue that partial manifestation of a trait should be regarded as being synonymous with full expression. Korey (1980), however, expresses doubts about this procedure, pointing out that all degrees of quasi-discontinuous expression are observable within any age group (Saunders and Popovitch 1978, Corruccini 1974).

Korey weighs up the scoring implications of the two-threshold and developmental noise theories as follows:

> . . . while the age progressive evidence weighs against the former thesis (because of the transitional role prominently borne by asymmetry), on the other hand neither does it imply perforce complete genetic equivalence between symmetry and asymmetry. In greatest likelihood the truth lies intermediate. What follows from this . . . is the disagreeable choice between a sampling stratagem which almost certainly introduces genetically extraneous information, and one which risks excluding genetically salient information.

Korey eventually decides in favour of sampling by individual as the most prudent course.

Perizonius (1979a), however, makes the valid point that asymmetrical presence of a trait may also be described as asymmetrical absence, the decision resting entirely on whether presence or absence of a feature is given a positive score. This statement is not entirely justified; where age studies denote a directionality to the trait expression (e.g. Korey demonstrates the increasing bilateral expression of supraorbital foramen with age) then unilateral presence should be regarded as such. There are several traits, however, in which directionality has not been, or cannot be established. The absence of the zygomaticofacial foramen, for example, is dependent on the presence or absence of the zygomaticofacial branch of the zygomatic nerve, and in such a case, the assignment of a positive or negative score is entirely arbitrary (the less frequent occurrence usually being scored positive).

If sampling by individual is the method of choice, the directionality of the trait must be known. For hyperostotic and hypostotic traits this presents little problem, but foraminal traits, among others, would have to be discarded. Pertinent here is the finding of Cheverud and Buikstra (1981, 1982) that the average heritability of foraminal traits is much lower than that of hyperostotic and hypostotic traits.

The uncertainty which must accompany the use of either of these two methods leads to the conclusion that Zegura's (1975) approach (scoring traits on one side only) is deserving

of reappraisal. The only real criticism that has been levelled at this method is that it ignores the information in the other side (Green, Suchey and Gokhale 1979). (Korey (1980) shows that their other assertion, that Zegura's method yields a less efficient statistic, is not necessarily correct). However, there is no reason why two distances (left side plus midline, right side plus midline) should not be derived for each of the sample pairs. Since there is little evidence of an overall preference for one side, as opposed to fluctuating asymmetry, in these traits (Perizonius 1979a), the two distances should be similar.

3.3.2. The mean measure of divergence: sources of error.

Like the metric Mahalanobis distance, the mean measure of divergence (MMD) for two groups is based on the difference between certain values which in some sense summarize the information in the data. The Mahalanobis distance is based on the difference in group means, the means being transformed to eliminate correlation and standardise the variances of the variables. The MMD uses trait incidence values, denoted by p, where the difference in the ps for each group forms the basis of the distance measure.

The use of p values creates difficulties, since the variance of p (p is an estimate of the population incidence P) is not constant from trait to trait. The p values can be regarded as independent binomial variables, whose variance is given by

$$\text{Var}(p) = \frac{P(1-P)}{N},$$

where N is the number of observations on which p is based. The population incidence P is unknown, but p is an unbiased estimate of P, and can be substituted in the above equation. It is clear from this equation that the variance is dependent on the value of p, becoming larger as p approaches 0.5, and diminishing as p approaches 0 or 1. Some method for stabilizing the variance is therefore necessary. This can be achieved by means of the Grewal-Smith transformation, which transforms the p values into θ values where

$$\theta = \arcsin(1 - 2p).$$

This transformation produces a variable whose variance depends only on the sample size, and the variance of θ is approximately 1/N. These transformed variables form the basis of the equation for the MMD.

Grewal (1962), at the suggestion of C. A. B. Smith, used the following expression to estimate the degree of divergence between sublines of inbred strains of mice.

$$MMD_{jk} = \sum_{i=1}^{R} [(\theta_{ij} - \theta_{ik})^2 - (1/N_{ij} + 1/N_{ik})] \; / \; R,$$

where R is the number of traits used, θ_{ij} is the transformed incidence of trait *i* in group *j*, and N_{ij} is the number of observations in group *j*. The expression $(1/N_{ij} + 1/N_{ik})$ represents the variance of the difference between the θs for the *i*th trait. This expression was subsequently employed by Berry and Berry (1967) and others (e.g. Kellock and Parsons 70a,b, Rightmire 1972, Corruccini 1974, Finnegan and Marcsik 1979). Grewal (1962) admitted that this measure is only one of many that may be used, since it is not based on sufficient statistics (Sjøvold 1973).

Green and Suchey (1976) demonstrated, however, that for small and moderate sample sizes, the variance of θ is not very close to 1/N, and this can lead to errors in the MMD. They showed that this error was particularly pronounced for the rarer traits, and investigated some alternative variance stabilising transformations. In conclusion, they recommended the Freeman-Tukey transformation as the superior statistic. Even this transformation, however, may be inadequate for the rarer traits. For incidences of 5% and 10%, sample sizes of more than 20 and 10 respectively are required if errors are to be avoided. This transformation is used in the present work, and its formula is as follows:

$$MMD_{jk} = \sum_{i=1}^{R} \left[(\theta_{ij} - \theta_{ik})^2 - \left(\frac{1}{N_{ij} + 0.5} + \frac{1}{N_{ik} + 0.5} \right) \right] / R,$$

where θ_{ij} is the transformation for the ith trait and jth group, given by the formula

$$\theta = 0.5 \,\mathrm{asin}[\, 1 - 2K / (N+1) \,] + 0.5 \,\mathrm{asin}[\, 1 - 2(K+1) / (N+1) \,],$$

where K is the count of positive observations and N the total number of observations for trait *i*.

Finnegan and Cooprider (1978), however, compared thirteen different equations for divergence, and found little variation in the results produced. They argue that the distance model resulting from the Grewal-Smith statistic is not inferior to the more sophisticated models, though the latter may be superior when sample sizes are small and trait incidence

low. Finnegan and Marcsik (1979) used this conclusion to justify retaining the simpler Grewal-Smith statistic in their study, but where computers are used to calculate the divergences, the extra complexity of the Freeman-Tukey equation should not be a deterrent.

A second source of error in the divergence arises because the MMD assumes that the individual traits are uncorrelated. Truslove (1961) demonstrated that this was true for the mouse, and Berry and Berry (1967) and Kellock and Parsons (1970a) did so for human samples. Corruccini (1974) questioned these findings, concluding from his own studies that the average correlation level, though not high, was significantly greater than zero and not lower than the average metric correlation. However, fewer significant associations (at $p < 0.05$) occurred than were expected by chance, suggesting that association, though greater than expected on the average, does not reach a detectable level in individual pairs. Nevertheless, preliminary analysis of trait correlations is of value, since highly correlated traits can be excluded, and errors arising from correlation minimised.

Finally, Sjøvold (1973) notes that errors arise in the MMD when different numbers of observations occur for different traits. Where sample sizes for bilateral traits are double those of midline traits, the bilateral traits have a greater weight and contribute more to the MMD since their variance estimate is smaller. MMDs between groups may not be strictly comparable if different traits have different weights in each distance measure.

3.3.3. Tests of significance.

Interpretation of the divergences is aided by a knowledge of the significance of these values. This is achieved by comparing the divergence to its standard error. The formula suggested by Sjøvold is used in this work (see Sjøvold 1973). As with the metric variables, significance levels should be used to assess the distances once the groups have been plotted.

3.3.4. Interpretation of the matrix of distances.

Interpretation of a matrix of MMD values is complicated by two factors:

1. The MMDs are not Euclidian distances, and,
2. The presence of negative values confuses the interpretation.

To overcome the first problem, Berry and Berry (1972, 1971) suggest using the square root of the MMD, a statistic (the Estimate of Divergence, Berry 1974) which, to a first approximation, fulfills the triangle inequality. This procedure, however, does not take into account that negative values for the MMD may be produced, especially when sample sizes are not based on the number of sides, since the smaller the sample size, the more likely that a negative MMD will be produced.

When a single large population is repeatedly sampled, the MMDs produced from each sample will have a *mean* value of zero. Berry and Berry (1972) therefore regard negative values as showing that there is no divergence between the populations. Berry (1974), when using the Estimate of Divergence, apparently converts negative MMDs to zero before taking the square root. This may lead to a loss of information, however, if all negative values are seen as equivalent - strictly, on this line of reasoning, all non-significant positive values should also be reduced to zero. Since the magnitude of positive values, as well as their significance, is considered instructive, then a large negative MMD should imply that the populations are even more similar than those with a small negative (or non-significant positive) value. It is likely, however, that large negative values will reflect the inadequacy of the sample sizes rather than population affinity.

For consistency with the approach for metric distances, MMDs are plotted using ordinal scaling. Since only the rank order of the distances is preserved using this method, the non-Euclidian nature of the divergences is of no consequence; neither is the presence of negative values, since a constant can be added to each distance to exclude negative values, without affecting the rank order. As with metric distances, the points should first be plotted, and the plots then interpreted in the light of significance tests.

4

MATERIALS AND METHODS.

The crania used in this study derive from two sources. First, seven samples represent the inhabitants of ancient Greece and Crete. Their small size and poor condition reflect the problems with which most anthropologists are faced when trying to extract statistically valid information from ancient remains. Secondly, five samples from ancient Egypt and one from recent Kenya, sufficiently large for the statistical testing of hypotheses, are studied. The sites will now be briefly described; their geographical positions are shown in maps A, B and C on the following pages, and their chronological relationships in figure 4.1.

4.1. Materials.

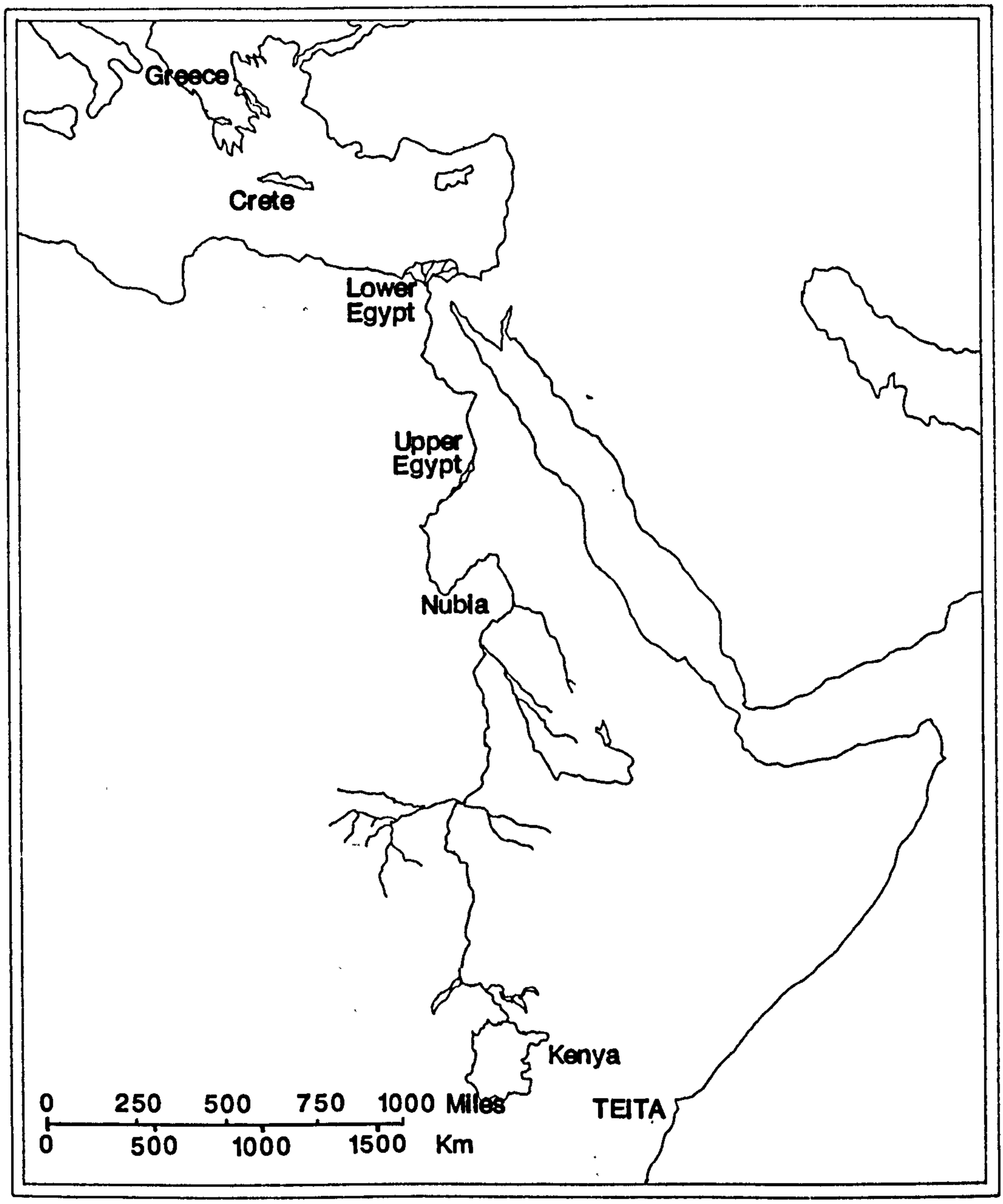
4.1.1. The Greek and Cretan sites.

These seven samples were studied in 1985 during six months of field work in Greece. In general, these samples were small and often poorly preserved, but measurements were taken and traits scored wherever possible, even from fragmentary remains. Unlike Egypt, whose hot arid conditions have preserved vast numbers of complete skeletons, Greece's climate and soil have not been kind to its interments. Angel (1945) states:

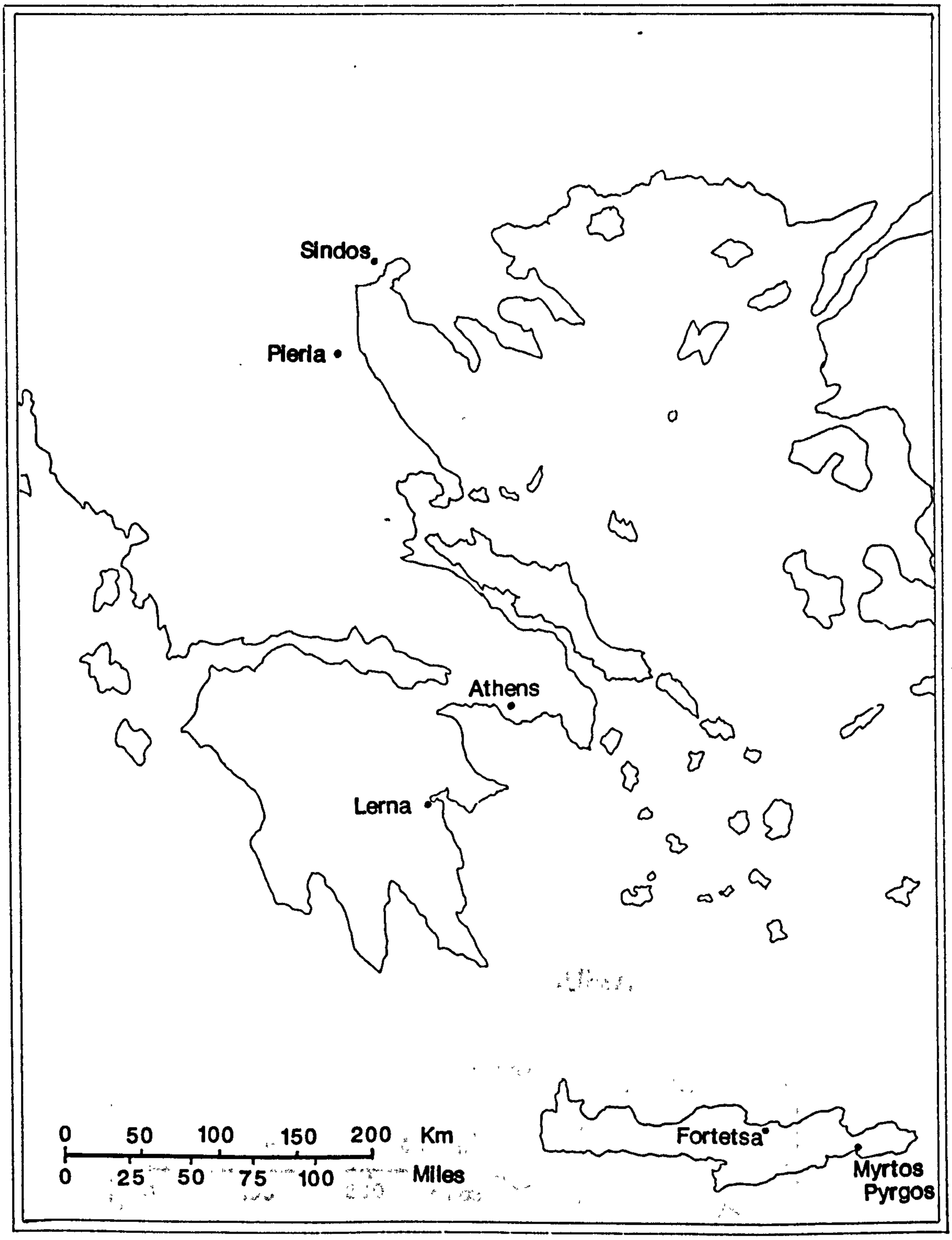
> Greek skeletal material is usually poorly preserved, being dissolved, warped, crushed and cracked by the alternate winter soaking of limey, clayey soil and summer baking and dry contraction of the soil.

Much time had to be spent on conservation before measurements could be taken. Even after painstaking reconstruction, the final sample sizes often remained pitifully small. Nevertheless, this is all the material that is available, and this study will attempt to extract the maximum information from it. The sites are presented in the order in which they were studied.

Map A. Geographical Origin of the Crania.



Map B. The Greek and Cretan Sites.



Map C. The Nile Valley Sites.

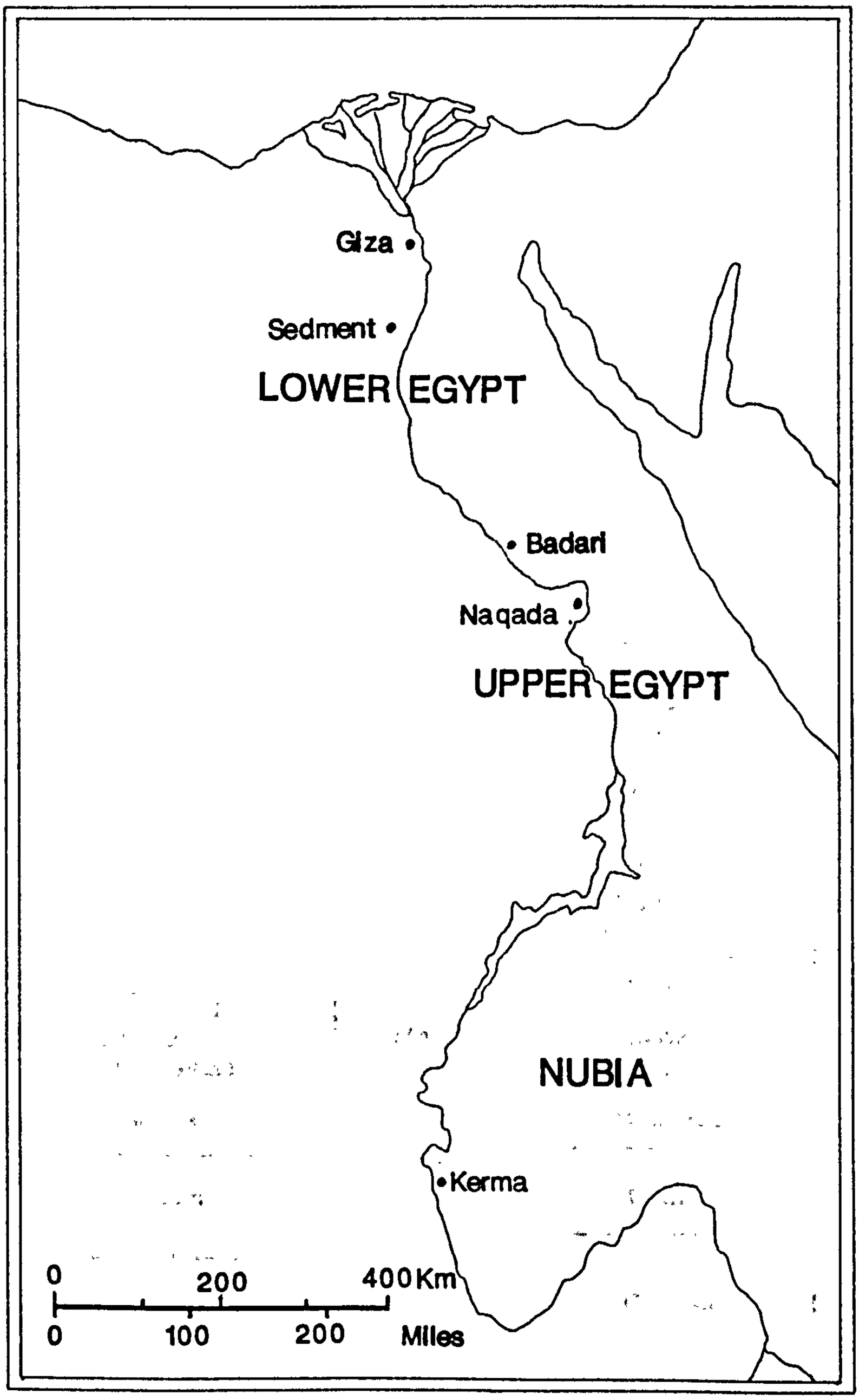


FIG. 4.1

CHRONOLOGY OF THE SITES.

Date B.C.	Egypt	Sites	Greece	Sites
5200	Neolithic			
5100				
5000	Early	[ ]		
4900	Predynastic	[ ]		
4800		[ ]		
4700		[ ]		
4600		[BADARI]		
4500		[ ]		
4400		[ ]		
4300		[ ]		
4200	Middle	[ ]	Neolithic	
4100	Predynastic			
4000				
3900		[ ]		
3800		[ ]		
3700		[NAQADA]		
3600		[ ]		
3500		[ ]		
3400	Late			
3300	Predynastic			
3200				
3100				
3000	1st Dynasty			
2900				
2800	2nd Dynasty			
2700			Early	
2600	3rd Dynasty		Helladic	
2500	4th Dynasty		I	
2400	5th Dynasty			
2300			Early	
2200	6th Dynasty		Helladic II	
2100	7th - 10th	[SEDMENT]	Early	
2000	11th Dynasty		Helladic III	{ }
1900				{ }
1800	12th Dynasty	[KERMA]	Middle	{ LERNA }
1700	13th Dynasty		Helladic	{ }
1600			I - III	{ [MYRTOS] }
1500	14th - 17th		Late Helladic	[PYRGOS]
1400	18th Dynasty		I - II	
1300			Late Helladic III	{ }
1200			(Mycenaean)	{ ATHENS-M }
1100	19th - 20th			{ }
1000			Sub-Mycenaean	
900	21st - 25th		Protogeometric	[PIERIA]
800	Dynasties		Geometric	{ }
700				{ ATHENS-G }
600			Archaic	{ }
500	26th - 29th	[ ]		[ ]
400	Dynasties	[GIZA]	Classical	[SINDOS]
300	30th Dynasty	[ ]		[ ]
200				
100 BC	Ptolemaic		Hellenistic	
0				
+100 AD				
+200	Roman		Roman	
+300				
+400				
+500				
+600	Christian		Christian	{ FORTETSA }

SINDOS (Classical-Hellenistic)

The site.

This cemetery, lying 15 miles west of Thessaloniki in northern Greece, was discovered accidentally in 1980 during construction work. Occupying a natural mound near the Gallikos river, it dates mainly from the Archaic and early Classical period (c. 550-450 B.C.). About half of the 121 graves were either cyst graves (lined with stone slabs) or sarcophagi of stone or clay. The remainder were rectangular pits, sometimes containing wooden coffins. A nearby hill shows signs of contemporary occupation; this may be the ancient town of Chalastra.

The grave goods include bronze, iron and many gold items. Many men were buried with their armour and weapons while the women's graves contained much gold jewellery. The large number of bronze and gold items found implies that these were a wealthy people. Gold face masks (recalling those buried in Mycenae, 1000 years earlier) were among the finds. Imported vases and clay figurines indicate trade with Attica, Corinth and the Aegean islands.

The skeletal remains.

34 crania	16 males. 18 females.

Most of the remains are from the Archaic-Classical cemetery; a few are from Hellenistic graves. While most of the cyst grave burials were very well preserved (though frequent flooding had led to green staining from the bronze grave goods) the earth burials were mainly fragmented and distorted. These fragments were strengthened by painting or soaking them with a solution of polyvinyl acetate (PVA) in acetone. The fragments were then glued together using an acetone-based glue. Gaps in the vault, if fairly small, were filled with sculptor's plaster, which was then carved to approximate the shape of the original bone and sanded smooth. Appropriately moulded plaster was also used to support the face where the buttress bones were missing.

Finally the reconstructed crania were aged, sexed (using post-cranial material where available), measured and scored. A few of the crania were distorted, but in these cases

approximations of the true values were made, with adjustments allowing for the distortion. A few cases of porotic hyperostosis were seen, but were not excluded from the analysis since sample sizes were so small.

PIERIA (Protogeometric)

The site.

Excavated in 1985, this site, near the northern slopes of Mount Olympus, consists of ten burial mounds dating from around 1000 B.C.

The skeletal remains.

26 crania	18 males.
	8 females.

These remains had to be cleaned of earth and conserved before they could be measured. The crania were remarkable both for their excellent state of preservation (14 whole skulls were present) and for their very poor teeth. Most of the specimens showed tooth loss, caries, heavy calculus and abscesses, even in the younger adults. One female, whose skull sutures indicated an age of 20, was completely toothless.

Fragmented crania were reconstructed in the same manner as those from Sindos. Two of the male crania showed sword cuts - probably the cause of death. One male showed hyperostotic thickening of the vault bones (10-11mm. thick over the parietals), but was nevertheless measured.

LERNA (Middle Helladic)

The site.

Lerna was excavated between 1952 and 1957 by Dr. J. L. Caskey of the American School of Classical Studies at Athens. The area appears to have been settled since Neolithic times (6th millennium B.C.). An impressive palace (The House of Tiles) and town wall was built during the Early Helladic II period. This palace was destroyed by fire around 2200 B.C. (as were many other sites in southern Greece), which fact has been widely interpreted as a sign of invasion. Afterwards, a tumulus of earth was erected over the burnt site. To Angel

(1971), this indicates " a strong element of the old population existing together with the conquerors."

The vast majority of the remains from Lerna belong to the Middle Helladic period (2000-1600 B.C.). These folk buried their dead in family groups beside their houses. They appear to have been fairly prosperous. Large amounts of imported pottery, especially Middle Minoan were found, indicating that trade and perhaps immigration flourished during the Middle Bronze Age.

The skeletal remains.

36 crania	25 males. 11 females.

These crania were stored at the American School of Archaeology at Corinth. They had deteriorated somewhat in the thirty years since Angel had studied them, so that the numbers available for study were reduced. Angel (1971) noted that these people showed great variability, even within family groups, which could indicate "contributions from several diverse populations."

ATHENS (Mycenaean - Archaic)

The site.

The Athenian Agora (market-place), in the shadow of the Acropolis, is a site that has yielded many remains spread across a wide time period. These remains, many of which were described by Angel (1945), are stored at the Agora Museum. From amongst those catalogued, two well separated time periods were devised for which an adequate number of well preserved remains were available. These were the Mycenaean-Submycenaean (circa 1400-1050 B.C.) and the Geometric-Archaic (c. 900-600) periods, called from now on Athens-M and Athens-G respectively.

ATHENS-M (Mycenaean-Submycenaean)

The skeletal remains.

28 crania	14 males. 14 females.

These remains are the contents of the Mycenaean chamber tombs surrounding the market-place.

ATHENS-G (Geometric Archaic)

The skeletal remains.

21 crania — 16 males
5 females.

These are the inhabitants of Geometric and Archaic graves from the Agora.

MYRTOS PYRGOS (Middle Minoan III - Late Minoan I)

The site.

On the hill of Pyrgos, east of the river Myrtos on the south-east coast of Crete, are the remains of a village dated to c. 1600-1450 B.C. It is dominated by a 'country house' (Cadogan 1986), whose inhabitants probably collected the taxes levelled by the rulers of the Minoan palaces. The site was excavated by G. Cadogan in 1970-1975. The skeletal remains came from a communal tomb and an ossuary situated in the heart of the village, behind the 'country house'.

The skeletal remains.

25 crania — 20 males.
5 females.

These skulls, though very poorly preserved, are good by Minoan standards. The remains, including the crania had previously been studied and measured by Dr. J. H. Musgrave.

FORTETSA (Early Christian)

The site.

The village of Fortetsa, near Knossos in Crete, was the site of this early Christian (c. 600 A.D.) osteotheke, a communal stone-lined bone pit. It was excavated in 1974 by Catling and Smythe (1976). A single early Christian female from a neighbouring site (KMF) was added to the sample to increase its size.

The skeletal remains.

11 crania — 5 males.
6 females.

The cranial measurements taken by Musgrave (1976) were used; non-metric traits were scored by the author.

4.1.2. The African sites.

These crania were studied at the Duckworth Laboratory, Cambridge in 1986. There are five ancient Egyptian samples, all large and well preserved. One modern sample (the Teita from Kenya) was also studied as an outlier to give perspective to the plots. Since there was not time to measure them, the measurements recorded by other workers were employed, though all non-metric traits were scored by the author. The sites are presented in chronological order.

BADARI (Early Predynastic)

The site.

Excavated in the 1920s by Caton-Thompson and Brunton, this site, consisting of several cemeteries and settlements, is the earliest known example of the Predynastic period. Thermoluminescence techniques (Whittle 1975) have dated the Badarian culture to between 3700 and 5500 B.C. Trigger (1982), however, maintains that dates earlier than 5000 and later than 4000 B.C. are unlikely. The cemeteries comprise individual circular or oval graves, the male and female graves often being segregated. Grave goods include pottery, beads and stone tools, and there is little difference in "richness" between burials. The settlements were clusters of rough shelters, yielding evidence of cereals, cattle, sheep and goats. The site as a whole probably represented the local early farming population.

The skeletal material.

58 crania 36 Males
22 Females

Sixty skulls and some post-cranial remains were originally recovered, though the records of the Duckworth Laboratory show that they "have deteriorated considerably since they were last measured." Non-metric traits were scored, though the hardened resin-like compound with which the skulls had been treated made the scoring of some foraminal traits difficult. The measurements made by Stoessiger (1927) were employed.

NAQADA (Middle and Late Predynastic)

The site.

This Predynastic culture is dated by radio-carbon methods to between 4000 and 3500 B.C. Excavated at the turn of the century by Flinders Petrie, it consists of simple pit graves, similar to those found at Badari. During the period of the Naqada culture, large settlements evolved, probably supported by intensive irrigation agriculture.

The skeletal material.

101 crania	50 males
	51 females

The Duckworth Laboratory contains some 500 specimens from this site, though many are now in a poor condition. The cranial measurements utilized were those taken by Fawcett (1902). The selection of the sample used here was largely random, though state of preservation was an important selection criterion.

SEDMENT (IXth Dynasty)

The site.

This site was excavated by Brunton and Petrie in 1920-21. The site, a large group of cemeteries, contained interments mainly from the IXth Dynasty (circa 2100 B.C., a period of approximately 90 years). The graves were rectilinear pits, containing unmummified bodies in plain wooden coffins. The grave goods (headrests, pottery, models of servants, occasional jewellery) were of similar type and quantity for most of the graves, indicating similar social status of the inhabitants, and there was no suggestion of foreign incursion into the population (Woo 1930). Petrie believed that they were the inhabitants of Herakleiopolis, 5 miles distant; they probably represent a moderately affluent section of the population.

The skeletal material.

68 crania	39 males
	29 females

Of the original 71 specimens presented to the Biometric Laboratory (and now in the Duckworth Laboratory), 69 boxes of crania remain, mostly in good condition. One specimen

was excluded because of immaturity. The cranial measurements taken by Woo (1930) were used; all non-metric traits were scored by the author.

KERMA (XII-XIIIth Dynasty)

The site.

Excavated between 1913 and 1916 by G. A. Reisner, Kerma, situated in the modern Republic of Sudan, dates from the XII-XIIIth Dynasties, circa 1800 B.C. There has been a long debate as to whether the inhabitants of Kerma were a pocket of Egyptians living in Nubia or Egyptianised natives (Nielsen 1973). Kerma seems originally (from the Ist to the XIth dynasty) to have been a trading station, at which periodic expeditions from Egypt called to collect and deliver goods.

The site consists of a massive mud brick-tower (the Western Deffûfa) and a large cemetery, only parts of which have been excavated. The function of the Western Deffûfa is unknown; Reisner (1923, cited by Collett 1930) thought it was built principally as a fortress and a stronghold for the protection of goods. During the XIIth Dynasty, native revolts caused Sesostris I to send a large military force to Kerma, under the leadership of Hepzefa. The latter is thought to have erected the Deffûfa, and have founded the Egyptian Cemetery, which remained in use for over 350 years. Reisner (Collett 1930) regarded the inhabitants of Kerma as Egyptians:

> After the advent of Hepzefa the number of colonists was not substantially, if at all, increased by the traders from Egypt . . . The tenure was a military one and it is unlikely that there was much intermarriage with native peoples of the locality.

An alternative interpretation (Trigger 1976) of the Deffûfa is that it was part of the palace of the "Kerma Ascendency", independent rulers who arose when the break-up of the Middle Kingdom political system led to Egypt's withdrawal from Lower Nubia. These rulers controlled the Nile trade and appear to have traded with the Asiatic 'Hyksos' people who ruled parts of Egypt during the turbulent Second Intermediate Period. With the reunification of Egypt and the expulsion of the Hyksos by the Pharaohs of the XVIIIth Dynasty, Nubia was reconquered and the Kerma Ascendency came to an end.

Whoever the inhabitants were, their burial customs were quite different from those of contemporary Egypt. The main peculiarity was the sacrificial burial, where in some cases as many as 320 people appear to have been buried alive with the body of their chief. This custom was prevalent in predynastic Egypt and in early Nubian graves. It was not only the rulers who practised this custom; even the poorer graves had one or two human sacrifices, though animal sacrifices replaced some or all of the humans in later graves. Bed burials (unknown in Upper Egypt at that time) were also common, as was the Egyptian practice of covering the body with a cowhide.

The skeletal material

84 crania	43 males 41 females

Skeletal material is mainly from a series of tumuli, and it is likely that the majority of the remains represent sacrifices. The origin of the sacrifices is unknown, but there is no reason to believe that they were necessarily prisoners of war or slaves. They could equally have been the valued servants of the chief, and may have come from a wide area, reflecting the cosmopolitan nature of a royal court (Hillson 1978)

Crania were selected, from over 300 taken from the site, on the basis of completeness. These specimens were previously measured by Collett (1930), whose data were used in this study. All non-metric traits were scored by the author; an additional 29 crania were scored to allow comparison with the set of 50 scored by A. C. Berry (Berry, Berry and Ucko 1967).

GIZA (XXVI-XXXth Dynasty)

The site.

This site was excavated by Flinders Petrie shortly after 1900. The remains were taken from a single cemetery located south of the Giza pyramids, representing the time period between 600 and 200 B.C. During this period, Egypt was increasingly controlled by foreign powers and this cemetery is thought to contain several foreign burials.

The skeletal remains.

107 crania	55 males 52 females

The crania selected, from a sample of over 1700, were those measured by W. W. Howells, as many as could be located. Howells' decision with regard to sex were accepted.

TEITA (Modern)

The site.

These skulls were collected by L. S. B. Leakey in 1929. The Teita, a small group of Bantu-speakers living in south-east Kenya, formerly exhumed the skulls of the dead after about 2 years and placed then in rock-shelters or caves, which thereby became ancestral shrines. Leakey was allowed to visit these shrines and remove the skulls of those with no living descendants, or whose relatives had been Christianised. They are believed to go back no further than three or four generations prior to their collection by Leakey.

The skeletal remains.

81 crania	34 males
	47 females.

These crania represent a single clan, at least in the male members. Though the females might be expected to be derived from other clans because the Teita practised exogamy, Howells (1973) found both sexes to be low in variability. Howells' judgement with regard to sexing was followed. Forty-nine female crania were scored, but two were omitted from the final analysis since their codes could not be located in Howells' measurement recording sheets (stored at the Duckworth Laboratory).

4.2. Methods: Collecting the data.

This section describes the measurements and non-metric traits used in the analysis, and describes measuring and scoring techniques.

4.2.1. The measurements.

The measurements chosen should cover the entire cranium and be known to be genetically meaningful. The set of 57 measurements prescribed by Howells (1973) were taken as a starting point. During 5 months of field study in Greece, as many of Howells' measurements as could be taken from the often fragmentary remains were recorded. The 5 samples from

mainland Greece were measured by the author. For the two Cretan samples, measurements taken on a previous occasion by Dr.J.H. Musgrave were employed, so that inter-worker error was, unfortunately, introduced into the study.

Similarly, for the African material, lack of time meant that the measurements taken by other workers had to be employed. Regrettably, the introduction of inter-worker error was not the only effect of this expedient; the problem of different schools of measurement was also introduced. The conventions used by these other workers were as follows:

Site	Convention	Worker	Reference.
Fortetsa	Howells	Musgrave	Musgrave 1976
Pyrgos	Howells	Musgrave	unpublished
Giza	Howells	Howells	Howells 1973
Naqada	Frankfurter Verständigung	Fawcett	Fawcett 1902
Kerma	Biometric Lab.	Collett	Collett 1933
Sedment	Biometric Lab.	Woo	Woo 1930
Badari	Biometric Lab.	Stoessiger	Stoessiger 1927
Kenya	Howells	Howells	Howells 1973

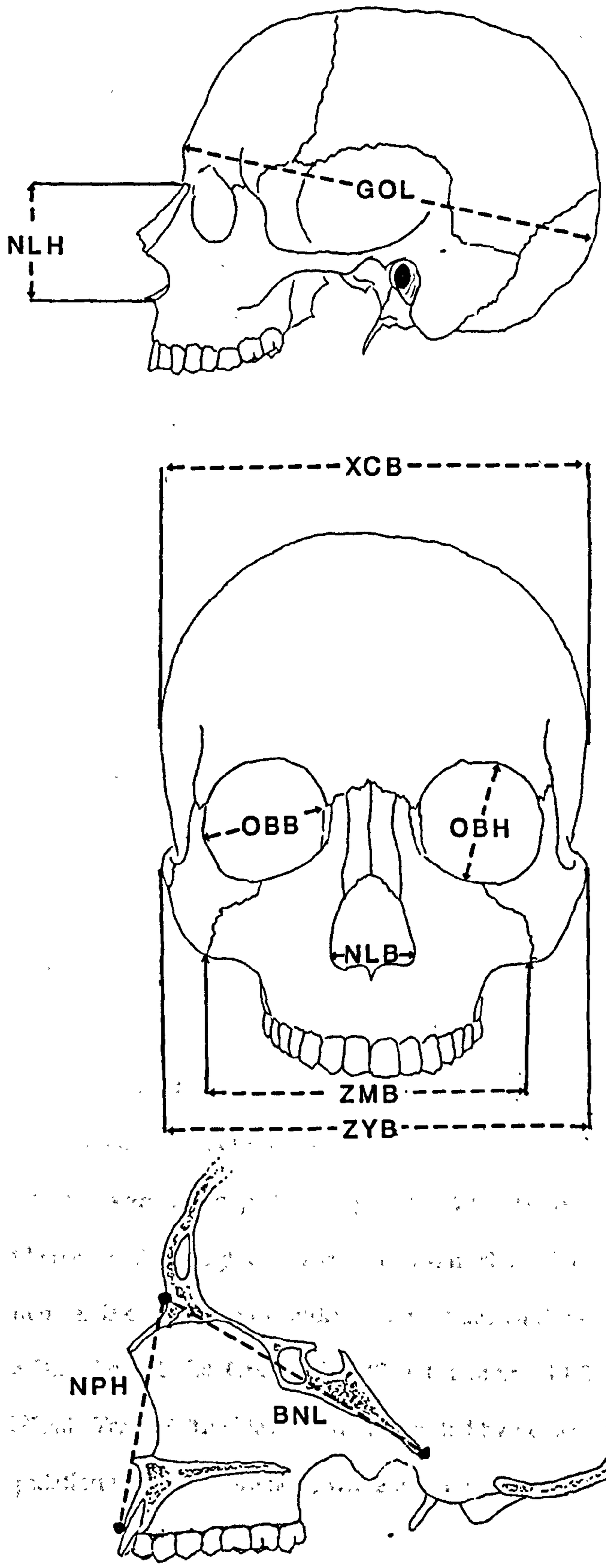
Since the Biometric Laboratory set of measurements grew out of the Frankfurter Verständigung, they will be treated as essentially the same measurements. The subset of these measurements which is synonymous with Howells' set (see Howells 1973, pp.170-187) was employed. These were already present on a computer database compiled by Dr. J. H. Musgrave at the University of Bristol.

Ten measurements were eventually employed. These are given below, using Howells' names, three-letter codes and descriptions. The synonymous Biometric Laboratory measurements are also noted. These measurements are illustrated in figure 4.2.

The measurements.

1. Glabello-occipital length (GOL) - *the greatest length, from the glabellar region, in the median sagittal plane.* This is synonymous with Biometric Laboratory's L, the greatest glabello-occipital length.
2. Basion-nasion length (BNL) - *the direct length between basion and nasion.* The Biometric Laboratory equivalent (LB- length of skull base) is not exactly the same since their definition of basion differs slightly from that of Howells, but the measurements "probably coincide in practice".
3. Maximum cranial breadth (XCB) - *the maximum cranial breadth perpendicular to the median sagittal plane (above the supramastoid crests).* The Biometric Laboratory version (B - maximum horizontal breadth) is defined as occurring only on the parietals, whereas XCB may occasionally lie on the temporal squamata. Although Howells does not accept B as a true synonym for XCB, Morant (1937) notes that in most Egyptian series, the maximum breadth is almost invariably found on the parietals anyway, so for the purpose of this study it is taken to be synonymous.
4. Bizygomatic breadth (ZYB) - *the maximum breadth across the zygomatic arches, wherever found, perpendicular to the median plane.* This is identical to J, zygomatic breadth.
5. Nasion-prosthion height (NPH) - *Upper facial height from nasion to prosthion.* Howells defines prosthion differently from all other schools. Nevertheless, the difference is likely to be very small, and rather than exclude all reference to a measurement which has been shown to be highly heritable, the Biometric Laboratory version, G'H (upper face height), was taken as being synonymous.
6. Nasal height (NLH) - *the average height from nasion to the lowest border of the nasal aperture on either side.* This is synonymous with Biometric Laboratory's nasal height (NH). Unfortunately, Woo (1930) records only NH', which measures to the base of the nasal spine; Howells remarks however that "the readings obtained should be virtually identical".

Fig. 4.2. The Cranial Measurements.



7. Orbital height (OBH) - *the height between the upper and lower borders of the left orbit, perpendicular to the long axis of the orbit and bisecting it.* Where the left orbit is damaged, the right side is used *for both diameters* as a best estimate of the values on the left. The Biometric Laboratory's O_2L is synonymous.

8. Orbital breadth (OBB) - *breadth from ectoconchion to dacryon, as defined, approximating the longitudinal axis which bisects the orbit into equal upper and lower parts.* This measurement has an Biometric Laboratory equivalent (O_1'L), but unfortunately, not all workers have used it. Fawcett (1902), for example, used the 'inner margin' of the orbit rather than dacryon (the measurement O_1L), while Collett records O_1'R only. Because of this confusion, orbital breadth was not included in the multivariate analyses.

9. Nasal breadth (NLB) - *the distance between the anterior edges of the nasal aperture at its widest extent.* The equivalent Biometric measurement is NB - nasal breadth.

10. Bimaxillary breadth (ZMB) - *the breadth across the maxilla from one zygomaxillare anterior to the other.* This is not the same as GB, where the lowest point of the zygomaxillary suture is taken as the landmark, though "it is probably close", and has therefore been included.

4.2.2. Non-metric traits - description and aetiology.

The sixty non-metric traits recorded in this work will now be described, as will the methods used in scoring them. The traits are listed in numerical order in table 4.1. For convenience, brief codes were devised to identify each of the traits; these abbreviations are also presented in table 4.1. The traits are also depicted in figs 4.3 to 4.12. Traits 1 to 30 are those used by Berry and Berry (1967), though Corruccini's (1974) method of scoring has been employed for some of them, as is outlined in the individual trait descriptions. Traits 31 to 60 have been taken from Ossenberg (1970), Czarnetzki (1971), Rightmire (1972), Corruccini (1974) and Perizonius (1979a). Trait 37, 'trochlear fossa', was noted by Le Double (1903) but has not been used in population studies before now, while trait no. 60, 'zygomatico-facial

TABLE 4.1

NON-METRIC TRAITS UTILISED IN THIS STUDY.

AND THEIR ABBREVIATIONS.

1. Highest nuchal line.	HiNuLin
2. Ossicle at lambda.	OsAtLam *
3. Lambdoid ossicle.	OsLambd
4. Parietal foramen.	FPariet
5. Bregmatic bone	OsBreg *
6. Metopism.	SuMetop *
7. Coronal ossicle.	OsCoron
8. Epipteric bone.	OsPter
9. Fronto-temporal articulation.	FrTemAr
10. Parietal notch bone.	OsPaNot
11. Ossicle at asterion.	OsAster
12. Auditory torus.	TorAud
13. Foramen of Huschke.	FHusch
14. Mastoid foramen exsutural.	FMasEx
15. Mastoid foramen absent.	FMasAb
16. Postcondylar canal patent.	CanConP
17. Bifaceted condyles.	BifaCon
18. Precondylar tubercle.	TubConA
19. Hypoglossal canal bridge.	BrCanHy
20. Foramen ovale and spinosum continuous.	FOvSpOp
21. Foramen spinosum open.	FSpOp
22. Accessory lesser palatine foramina.	FLPalAc
23. Palatine torus.	TorPal *
24. Maxillary torus.	TorMax
25. Zygomatico-facial foramen absent.	FZyFAb
26. Supraorbital foramen complete.	FSupOrb
27. Frontal notch or foramen.	FNotFr
28. Anterior ethmoid foramen exsutural.	FAEthEx
29. Posterior ethmoid foramen absent.	FPEthAb
30. Accessory infraorbital foramen.	FIOrbAc

* - Midline trait

TABLE 4.1 CONTINUED.

NON-METRIC TRAITS UTILISED IN THIS STUDY.

AND THEIR ABBREVIATIONS.

31. Inca bone	OsInca *
32. Infraorbital suture	SulOrb
33. Nasal sill sharp	NasSill
34. Nasal foramen	FNasal
35. Cribra orbitalia	CribOrb
36. Trochlear spur	SpurTro
37. Trochlear fossa	FosTro
38. Frontal grooves	GrFront
39. Squamo-parietal ossicles	OsSqPar
40. Os Japonicum trace	SuJapTr
41. Processus marginalis	ProcMar
42. Zygomatico-temporal foramen	FZyTem
43. Zygomatico-orbital foramen	FZyOrb
44. Occipito-mastoid ossicle	OsOcMas
45. Intermediate condylar canal	CanConI
46. Postcondylar tubercle	TubConP
47. Jugular foramen bridge	BrJugF
48. Pharyngeal tubercle	TubPhar *
49. Pharyngeal fossa	FosPhar *
50. Foramen ovale incomplete	FOvOp
51. Foramen of Vesalius	FVesal
52. Pterygo-basal bridge	BrPtBas
53. Pterygo-spinous bridge	BrPtSp
54. Spino-basal bridge	BrSpBas
55. Foramen ovale spine	SpinFOv
56. Accessory foramen spinosum	FSpAc
57. Lateral pterygoid perforated	PerfPt
58. Pterygoid spurs	SpurPt
59. Palatine bridge	BrPal
60. Zygomatico-facial foramen multiple	FZyFMu

* - Midline trait

foramen multiple', is a less ambiguous form of Czarnetzki's 'zygomatico-facial foramen double'. Trait 50, 'foramen ovale incomplete', was suggested by Wood-Jones (1931a). To avoid needless repetition, the numerous citations of Berry and Berry, Ossenberg, Perizonius, Wood-Jones and Corruccini, unless otherwise stated, refer to Berry and Berry (1967), Ossenberg (1970), Perizonius (1979a), Wood-Jones (1931a) and Corruccini (1974).

For convenience, the traits are grouped into categories, as suggested by Ossenberg, on the tentative basis of common aetiology. Sutural ossicles, sometimes classed as hypostotic traits, are here grouped separately. A final miscellaneous category holds those traits which are 'incertae sedis'. The categories are:

1. Sutural Ossicles
2. Hypostotic traits
3. Hyperostotic traits
4. Foraminal traits
5. Miscellaneous traits

1. Sutural Ossicles.

2. Ossicle at lambda.
3. Lambdoid ossicle.
5. Bregmatic bone.
7. Coronal ossicle.
8. Epipteric bone.
10. Parietal notch bone.
11. Ossicle at asterion.
31. Inca bone.
39. Squamo-parietal ossicle.
44. Occipito-mastoid ossicle.

Sutural ossicles (also called Wormian bones), are irregular isolated bones occurring in the course of the sutures. Figures 4.3, 4.4 and 4.6 depict the various types of ossicle. They occur most commonly in the lambdoid suture and are occasionally found at the fontanelles and at pterion. They arise from independent centres of ossification and usually include the whole thickness of the cranial wall, but occasionally involve only the inner or outer table (El-Najar and Dawson 1977). Pendergrass et al. (1956) note that "sutural and fontanelle bones are preformed in membrane and seemingly arise from detached portions of the primary ossific centres of the larger and related bones".

In contrast, Inca bones (classed here with sutural ossicles) develop when the several centres of ossification of the interparietal part of the occipital bone fail in part or in whole to coalesce with the supraoccipital part (Anderson 1983). This feature should, perhaps, be classed as a hypostotic trait (representing a deficiency of bony development) since accessory

centres of ossification are not involved. Different types of Inca bone are illustrated in figs. 4.3 and 4.4.

Ossicles are found more commonly in the complex sutures and, in the present series, it was noted that in skulls whose lambdoid suture was very complex, up to a dozen small slender ossicles were present on each side among the interdigitations of the occipital and parietal bones.

There is much disagreement about the relative contribution of genetic and environmental factors in the aetiology of these traits. Hess (1946) cited cases of wormian bones found in congenital and early-acquired hydrocephalics. He found correlations between these bones and asymmetry of the skull, malformations of the occiput and sphenoid, metopism and congenital anomalies of the CNS. This led him to claim that ossicle presence is a reaction to hypostosis (i.e. an insufficiency of osseous development) related to an inherited metabolic disorder. Torgersen (1954), through pedigree studies, showed that sutural variations are inherited as a dominant trait with incomplete (about 50%) penetrance and a variable expression.

El-Najar and Dawson (1977) noted the presence of lambdoid ossicles in several fetal skulls, and hypothesised that they are under the direct control of genes which allow the formation of secondary centres of ossification. They studied culturally deformed and undeformed crania and found that, though the *incidence* was unaffected, the *number* of bones was significantly higher in the deformed crania, and on the affected side of asymmetrically deformed skulls. To account for this, they state:

> Pressure exerted on the skull . . . appears to inhibit normal bone ossification and thus more wormian bones may be produced to fill in the gap between the sutures.

Their work contradicts the earlier finding of Ossenberg that cultural deformation does affect the incidence of Wormian bones. She found a higher incidence of posterior wormian bones in deformed skulls, while in the lateral vault where the skull was "free to expand and meet the growth demands of the brain" the incidence was lower than in the control series.

Fig. 4.3 Non-metric traits. Skull : posterior aspect.

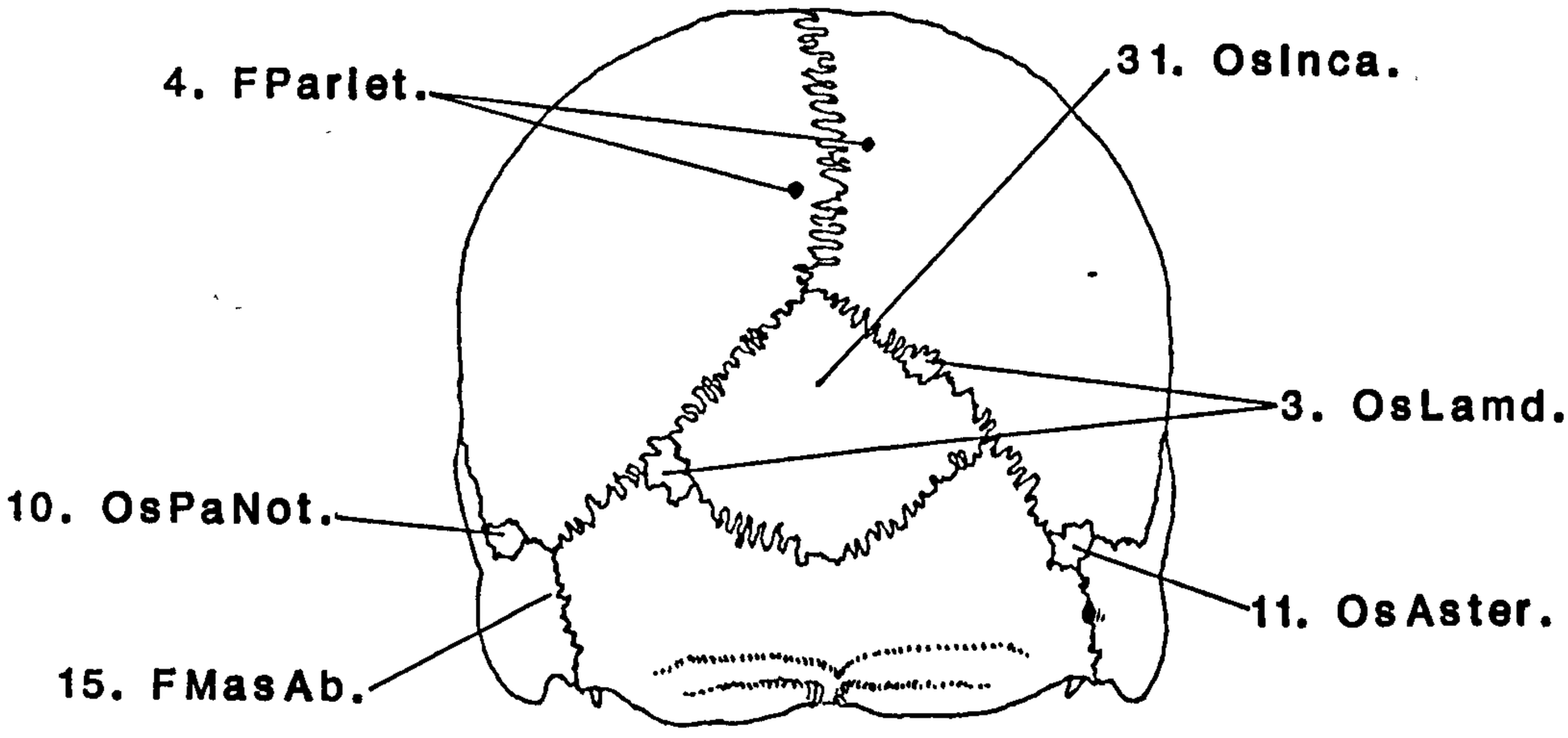
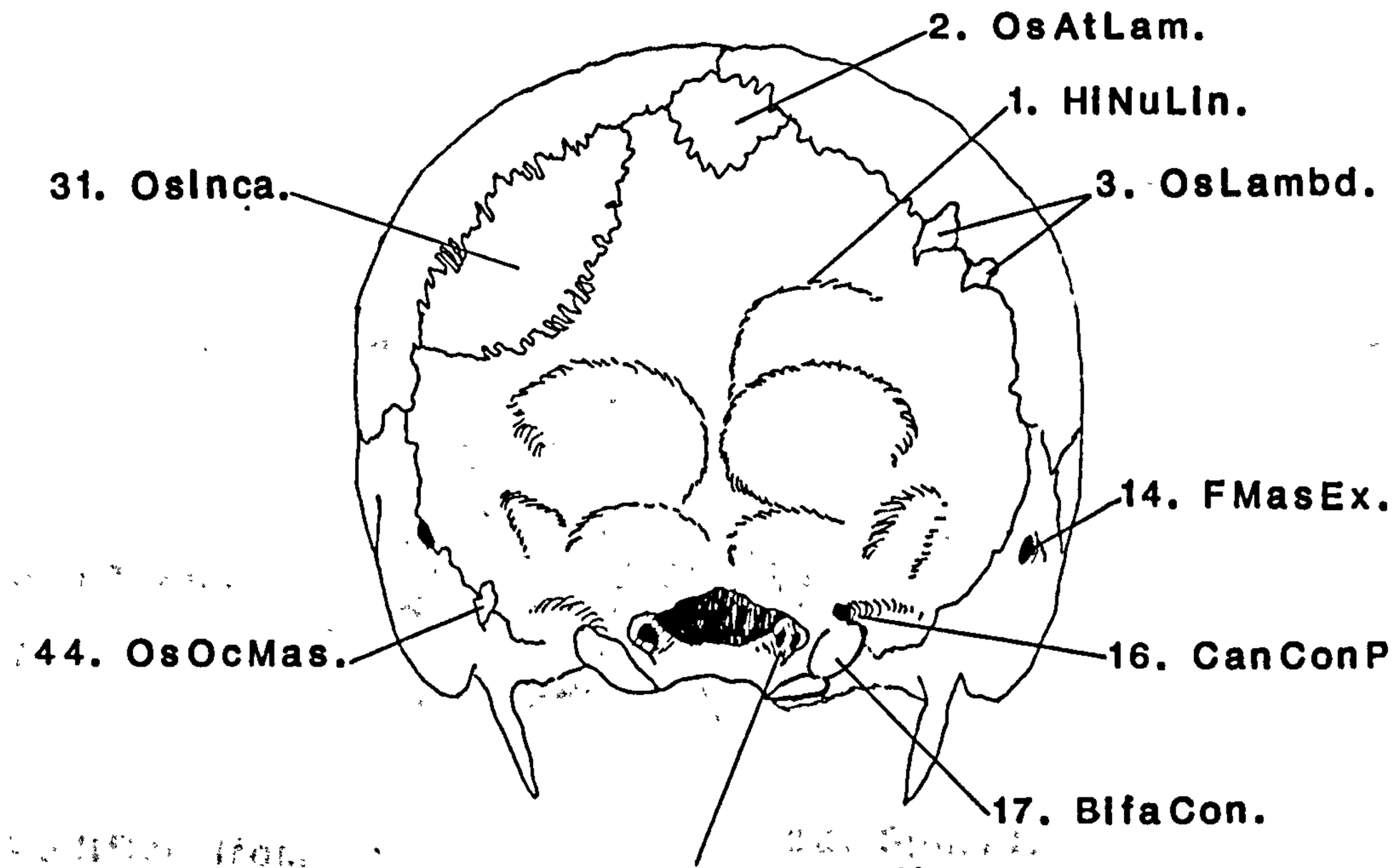


Fig. 4.4 Non-metric traits. Skull : infero-posterior aspect.*



* Modified from Berry and Berry, 1967.

Fig. 4.5 Non-metric traits. Skull : anterior aspect.*

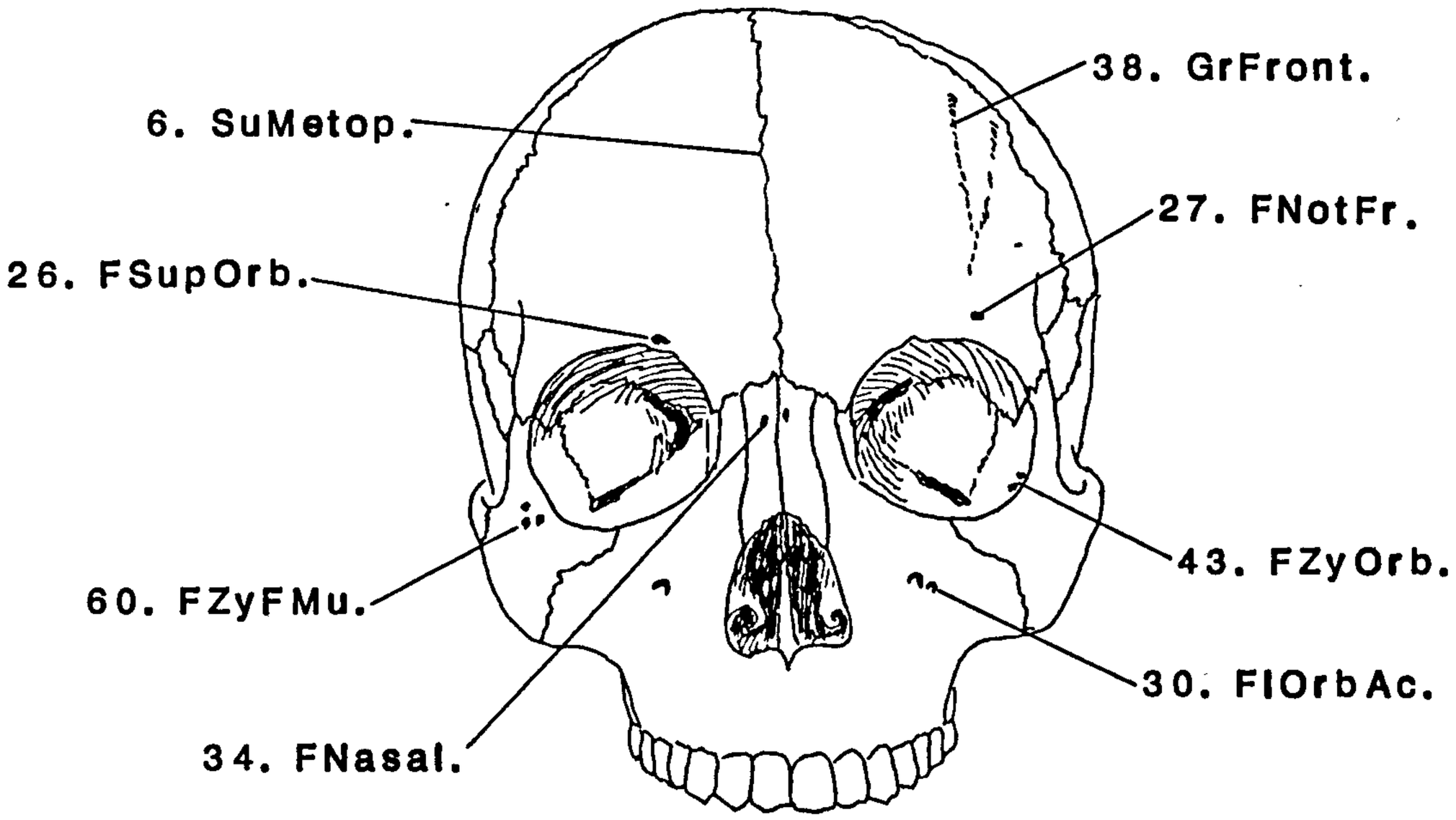
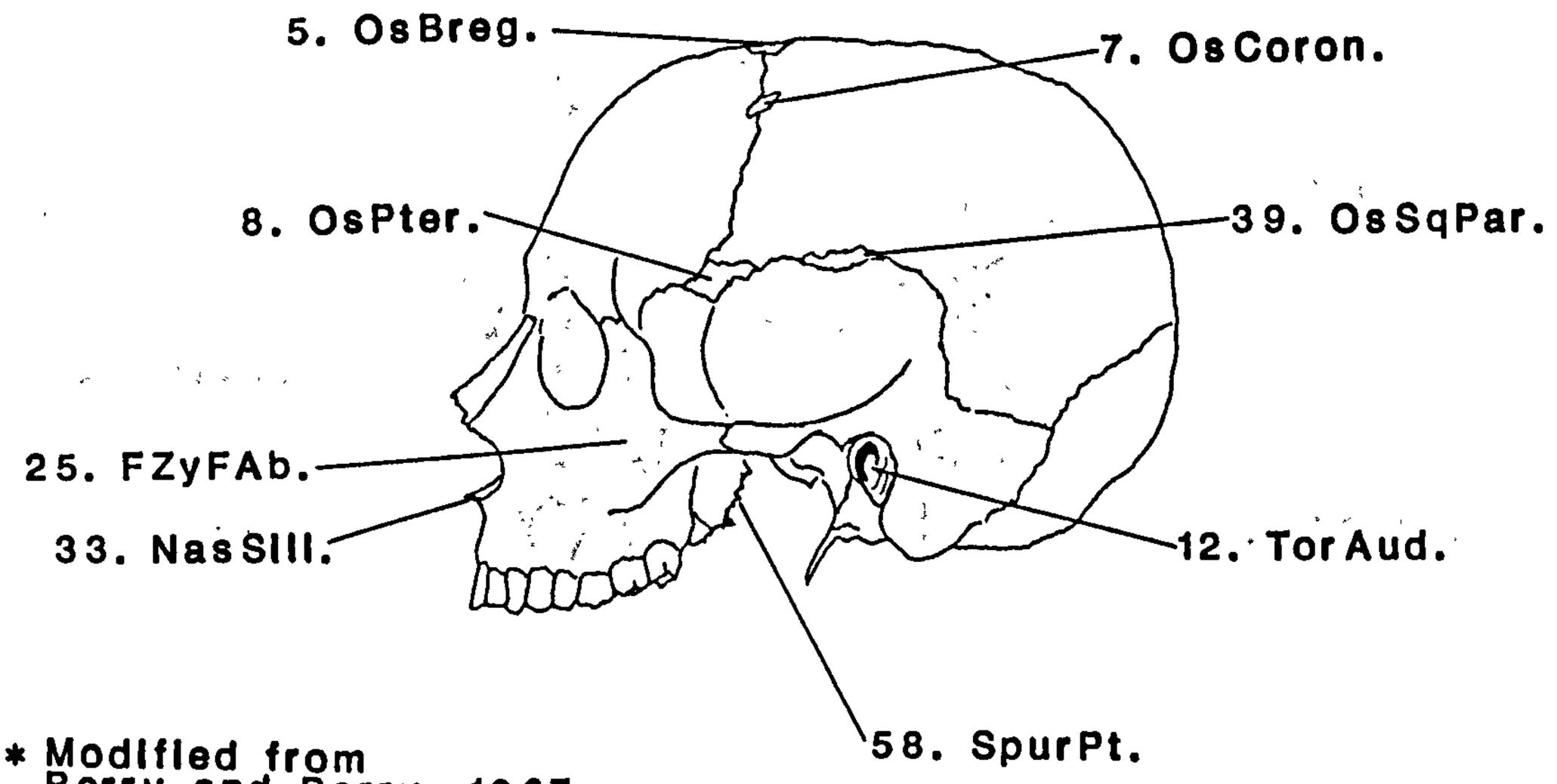


Fig. 4.6 Non-metric traits. Skull : lateral aspect.*



* Modified from Berry and Berry, 1967.

Fig. 4.7 Non-metric traits.

Orbital region : antero-lateral aspect.*

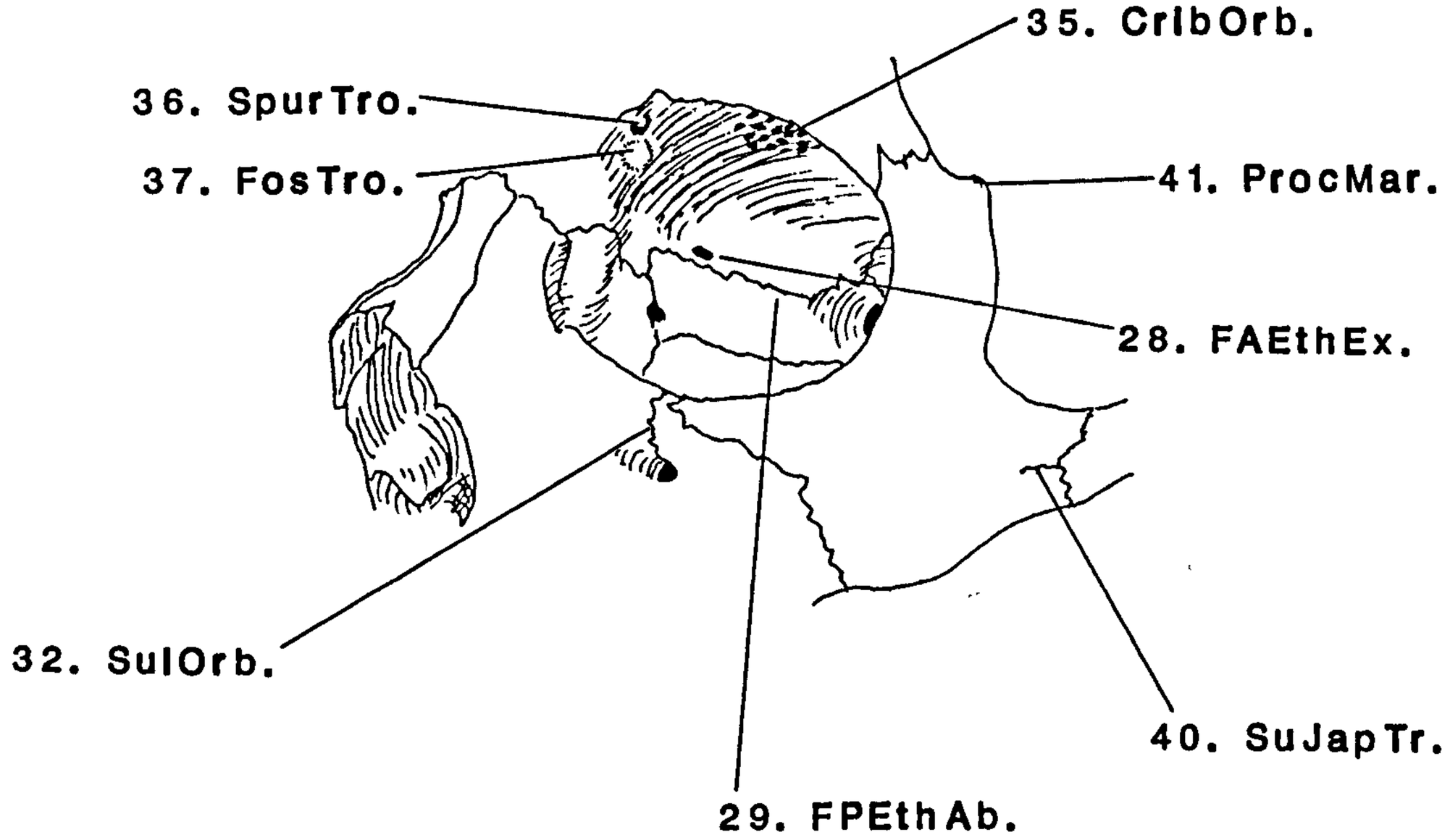
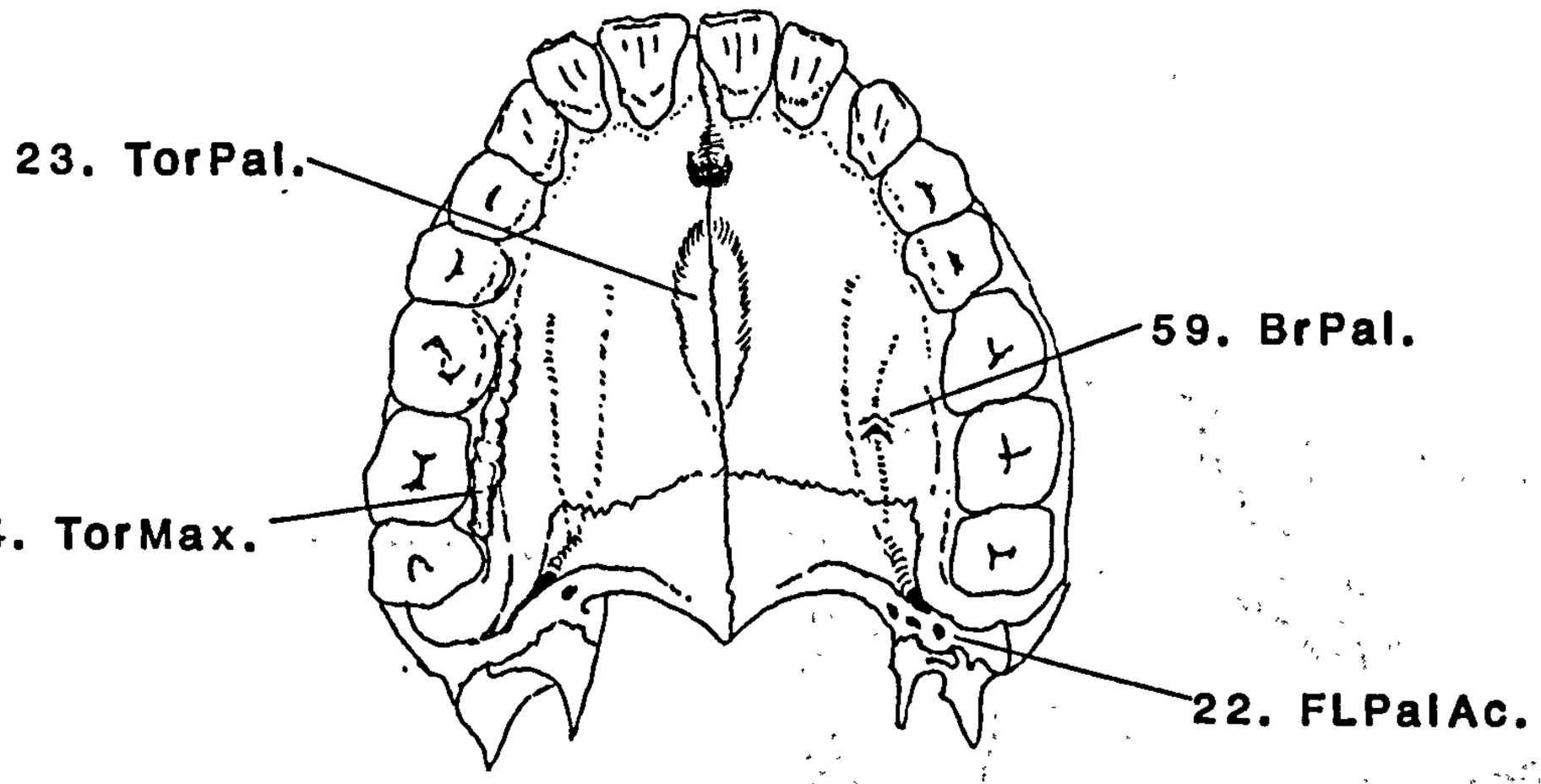


Fig. 4.8 Non-metric traits. Palatal region : Inferior aspect.



* Modified from Berry and Berry, 1967.

Fig. 4.9 Non-metric traits. Skull base : Inferior aspect.

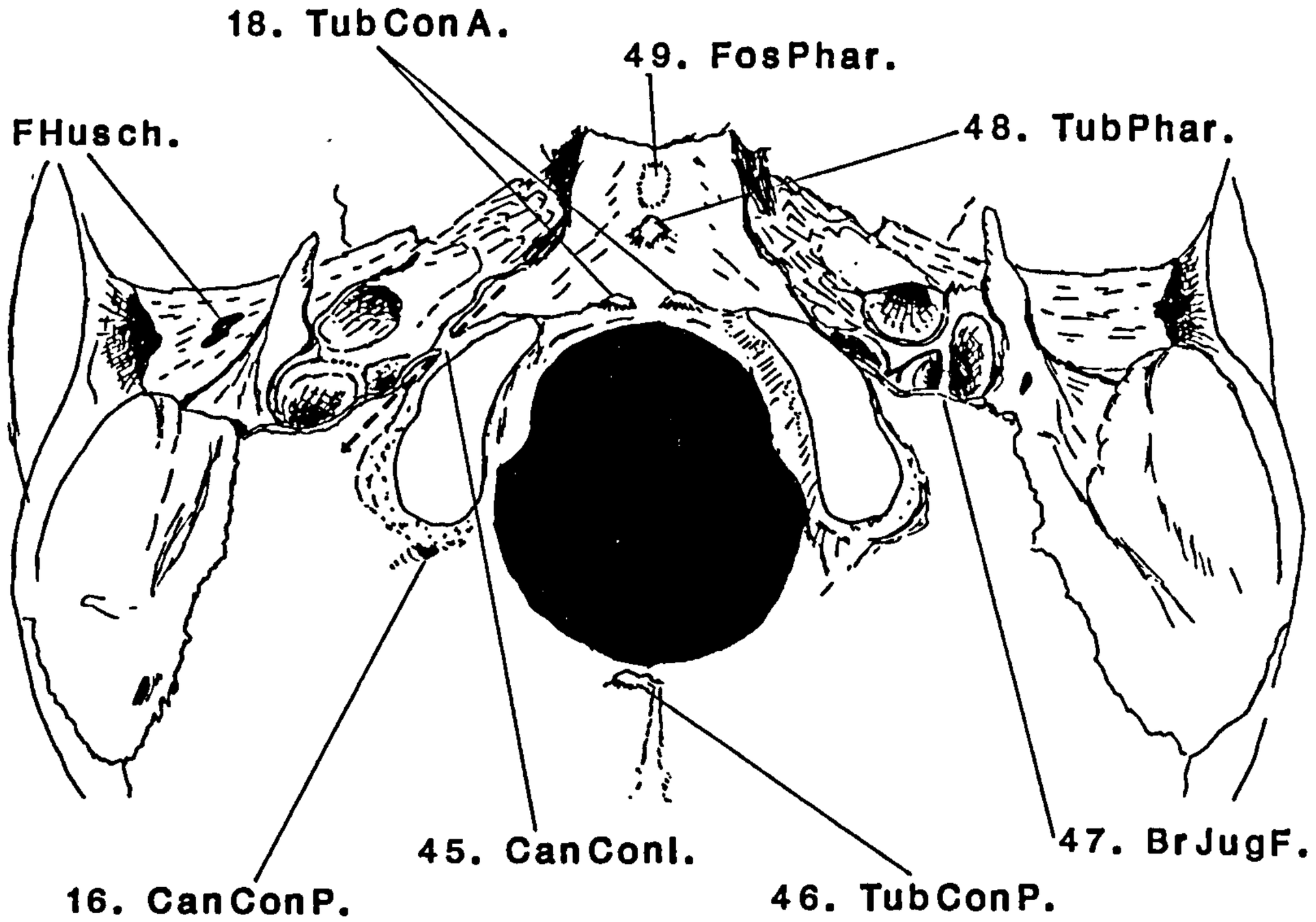
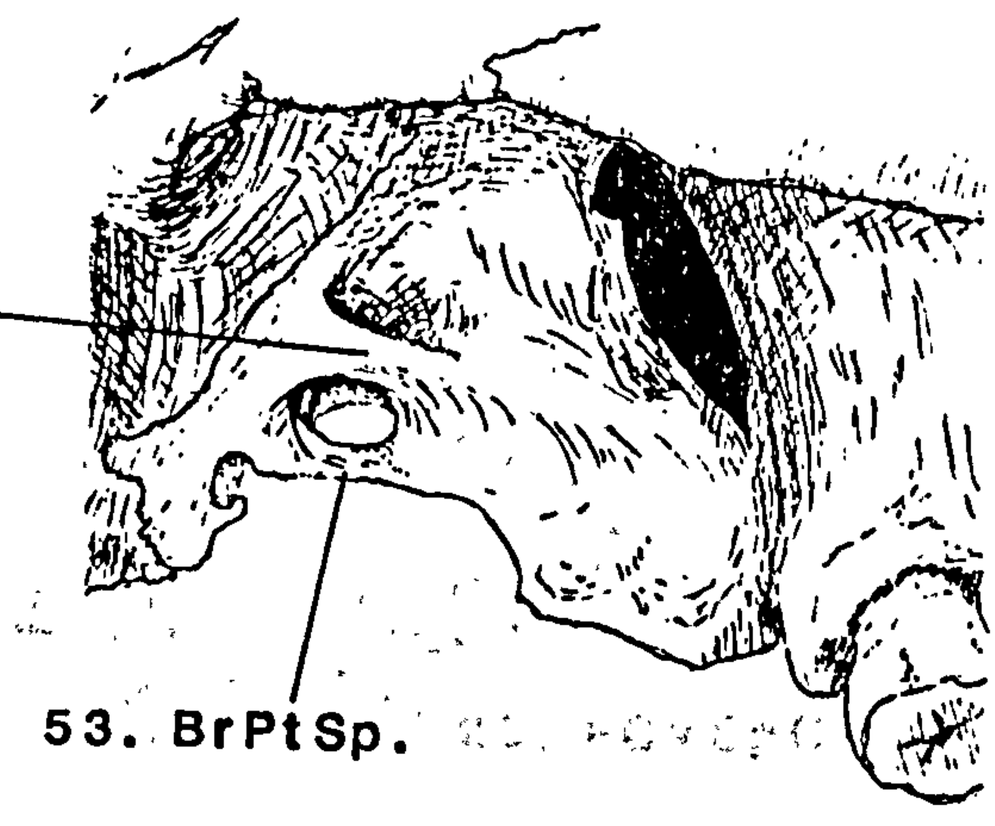


Fig. 4.10 Non-metric traits. Pterygoid : lateral aspect.*



* Modified from Chouke, 1947.

Fig. 4.11 Non-metric traits.

Temporal fossa :

postero-lateral aspect.

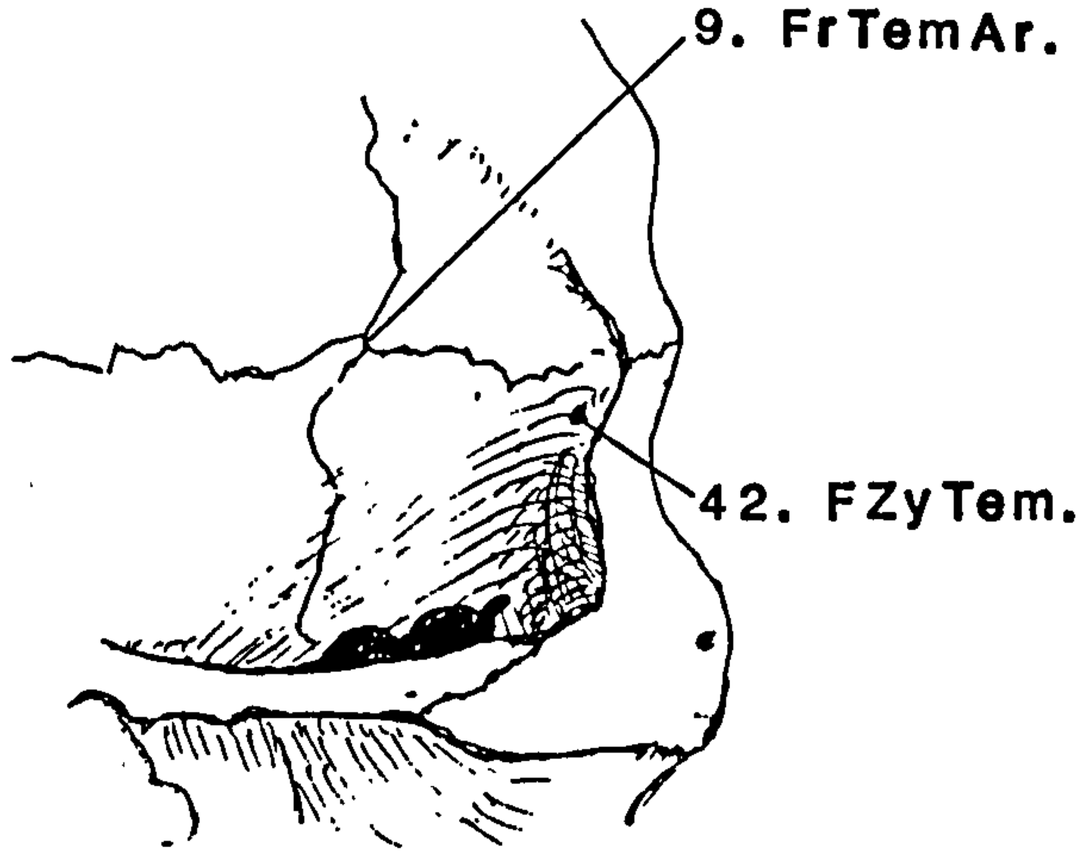
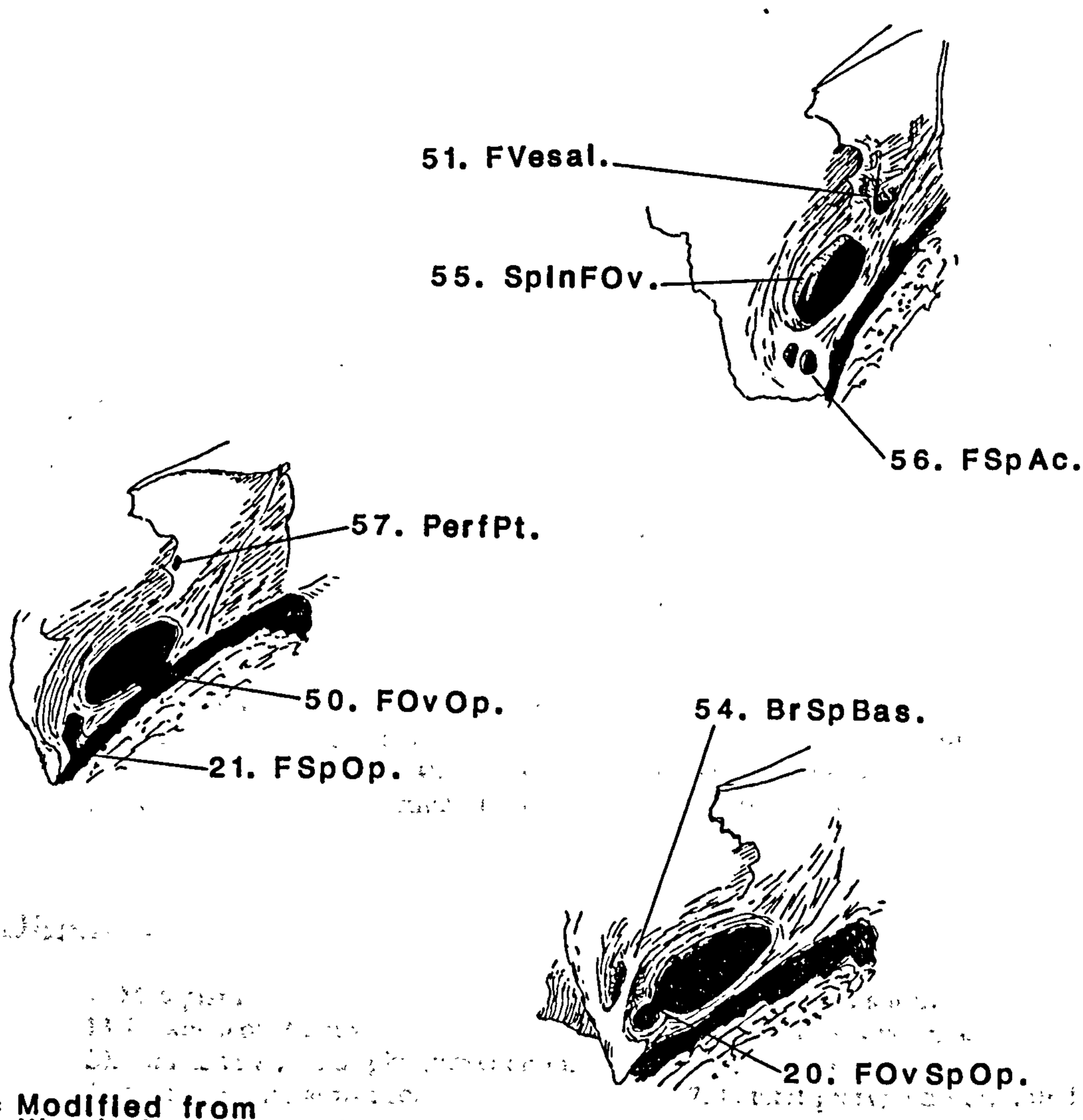


Fig. 4.12 Non-metric traits. F. ovale region : inferior aspect.*



* Modified from Wood-Jones, 1931b.

Bennet (1965) argued against the notion that wormian bones are under direct genetic control and suggests that they are secondary sutural characteristics brought about by stresses caused by growth rate differentials. He found, in three racial groups, that skulls with wormian bones had significantly shorter basioccipital lengths, and postulated that the ossicles are a response to stress when growth at the lambdoid suture is inhibited by retarded growth rate at the spheno-occipital synchondrosis.

Ossenberg questioned Bennet's inference that basioccipital length influences ossicle formation, noting that the reverse could equally be true. She draws attention to the danger of inferring causality from correlation; however, there would be little point in investigating correlations if no attempt were made to link then to causative factors. If basioccipital growth and the presence of sutural bones do represent cause and effect, then Bennet is probably correct, since growth of the chondrocranium, as discussed in chapter 2, is less sensitive to environmental fluctuation (has a higher heritability) than membrane bone growth (Van Limborgh 1970).

In conclusion, the presence of sutural ossicles may well be attributable to genetic factors, but the environment appears to play a role in their expression if not in their cause. If El-Najar and Dawson (1977) are correct in their belief that sutural stresses affect the number present but not their incidence, the scoring method used here accurately reflects the genetic basis of the traits. Inca bones may have a different aetiology since they mark the failure of ossification centres to fuse rather than the presence of accessory centres.

Scoring: (For all traits)	Sutural ossicles absent	- 0
	One or more ossicles present	- 1

Scoring is difficult in older specimens where the sutures may be wholly or partly obliterated. Very large single lambdoid ossicles are difficult to distinguish from lateral Inca bones (see fig. 4.4); in this study only large ossicles involving the median part of the interparietal portion of the occipital are classed as Inca bones.

2. Hypostotic Traits.

6. Metopism.
13. Foramen of Hüschke.
20. Foramen ovale and spinosum continuous.
21. Foramen spinosum open.
32. Infraorbital suture.
35. Orbital osteoporosis.
50. Foramen ovale incomplete.
57. Lateral pterygoid perforated.

Ossenberg describes hypostotic traits as those which represent a relative insufficiency of osseous development. Most of them represent arrested morphogenesis i.e. the retention of a fetal or infantile stage, as with metopism and foramen of Hüshcke. Ossenberg claims that these hypostotic traits show a slight preference for the right side, owing to the retardation of ossification on this side compared with the left (Torgersen 1951c), and that they follow an age regressive pattern up to a certain age, after which they are stable. Sex is also an intrinsic factor, women in general retaining more infantile characters than men.

6. Metopism.

The frontal bone develops from two primary centres of ossification (in the region of the frontal tuberosities) in fibrous tissue. At birth the bone consists of two halves separated by the metopic suture. Union begins in the second year of life and by the eighth year, the suture is usually obliterated. Torgersen (1951b) proposed that retention of the suture in adult life was caused by a dominant gene with varying penetrance.

Scoring:
Suture absent or trace present - 0
Complete suture present - 1

Corruccini classed traces of the metopic suture just above nasion as partial manifestations. These traces were recorded, but classed as absent when used in the analyses.

13. Foramen of Hüschke.

The tympanic ring in the neonate grows laterally to form a cylindrical structure, the tympanic part of the temporal bone. This growth does not take place at an even rate all around the ring but most rapidly in its anterior and posterior portions. These outgrowths meet and blend and thus, for a time, an opening exists in the floor of the meatus, the foramen of Hüschke. This opening usually closes around the fifth year but may persist throughout life (Williams and Warwick 1980). Ossenberg noted a rapid decrease in the incidence of this trait between 8 and 12 years, after which it remained stable. The trait sometimes takes the form of a cribriform defect. Perizonius and Ossenberg score this manifestation as present.

Scoring:
Tympanic plate complete - 0
Foramen or cribriform defect - 1

20. Foramen ovale and spinosum continuous.

This is synonymous with the trait 'foramen ovale incomplete' of Berry and Berry, though their term is used to describe a different trait in this series. The middle meningeal artery and meningeal branch of the mandibular nerve pass through the f. spinosum while the f. ovale transmits the mandibular nerve and accessory meningeal artery. These two foramina may communicate by a narrow chink or suture, or the postero-lateral wall may be completely misssing (Wood-Jones 1931a).

Scoring:	Postero-lateral wall complete	- 0
	Wall breached or missing	- 1

21. Foramen spinosum open.

The posterior wall of the f. spinosum is sometimes deficient. Wood-Jones classes the various forms of this trait. The posterior wall may be complete above but incomplete below (near the spine) or complete near the spine and incomplete as it passes into the cranial cavity. It may also be complete above and below but open in the middle. Alternatively, the f. spinosum may be represented only by a deep and elongated incisura on the angular region of the alisphenoid, communicating with the spheno-petrous fissure; Wood-Jones terms this last condition 'pithecoid'.

Scoring:	Posterior wall partial or complete	- 0
	Posterior wall entirely absent	- 1

32. Infraorbital suture.

During fetal development a fissure forms in the floor of the orbit beneath the infraorbital nerves and vessels. This fissure later forms the infraorbital canal. Its path of descent is marked on the facial surface of the neonate's maxilla by a suture extending from the orbital margin to the infraorbital foramen. This suture is usually obliterated a few years after birth, but may persist into adulthood. Ossenberg found that this trait tends to decrease in incidence with age.

Scoring:	Suture absent or trace present	- 0
	Complete suture present	- 1

Corruccini classes this trait as partially complete when the suture is visible but does not reach the infraorbital foramen. He also notes that it may originate at the

foramen but fail to reach the orbital margin. Both forms have been classed here as 'trace'.

35. Cribra orbitalia.

The use of cribra orbitalia (orbital osteoporosis) as a racial trait was first suggested by Welcker (1888, cited by Akabori 1933). He scored this sieve-like appearence of the bone in the orbital roof as pronounced, medium or faint. Akabori examined the trait in 400 Japanese skulls and found a considerable age influence, concluding that it was "a 'post-embryonic', rather than a racial phenomenon."

Hengen (1971), noting its association with porotic hyperostosis in the vault bones (diagnostic of blood disorders), suggested that it was caused by anaemia. Cybulski (1977) showed that immature individuals were far more affected than adults, and the incidence in females was three-times that in males. Since these two groups are prone to iron-deficiency anaemia in modern populations, Cybulski concluded that cribra orbitalia is a consequence of anaemia, though he did not rule out genetic factors related to blood disorders. This trait has been used recently by Corruccini (1974) and Kaul, Anand and Corruccini (1979). It has therefore been recorded, though its use as a population discriminator cannot be recommended.

Scoring:	Absent or faint traces	- 0
	Medium or pronounced	- 1

50. Foramen ovale incomplete.

Wood-Jones catalogues the variety of form shown by the foramen ovale. "It may be absent as a foramen by remaining confluent with the foramen lacerum medium", the condition seen in tarsiers, or "represented by any degree of completeness from a mere notch to an almost complete foramen encircled in over two thirds of its periphery by the alisphenoid", the condition prevalent in most monkeys and apes.

Scoring:	F. ovale separate from f. lacerum	- 0
	F. ovale confluent with f. lacerum	- 1

57. Lateral pterygoid perforated.

This trait is described by Corruccini as "a true foramen between the superior and inferior pterygoid spines". Sometimes a foramen was seen near the posterior egde of the pterygoid, which appeared to be formed by the coalescence of two pterygoid spurs. Whether this would constitute a 'true' foramen according to Corruccini's criteria is not clear, but it was scored as such.

Scoring:	Perforating foramen absent	- 0
	Perforating foramen present	- 1

3. Hyperostotic Traits.

Fifteen of the traits studied may be regarded as hyperostotic; these may be further classified as bridging traits, tubercles and spurs, and exostoses.

BRIDGING TRAITS:

45. Intermediate condylar canal
52. Pterygo-basal bridge
53. Pterygo-spinous bridge
54. Spino-basal bridge
59. Palatine bridge

TUBERCLES AND SPURS :

18. Precondylar tubercle
36. Trochlear spur
41. Processus marginalis
46. Postcondylar tubercle
48. Pharyngeal tubercle
55. Foramen ovale spine
58. Pterygoid spurs

EXOSTOSES:

12. Auditory torus
23. Palatine torus
24. Maxillary torus

Hyperostotic traits, as defined by Ossenberg, are generally characterised by an excess of ossification over the non- anomalous condition. In some cases, bone may extend into adjacent structures of cartilage, ligament or membrane. Ossenberg found that many of these traits followed an age- progressive pattern, at least until adulthood, and were, in general, more commonly found in male skulls and on the left side.

BRIDGING TRAITS.

These are bony extensions into ligaments or the fibrous tissue surrounding blood vessels.

45. Intermediate condylar canal.

The intermediate condylar canal is formed by the bridging of a gutter which lies immediately lateral to the occipital condyle. This gutter transmits a venule which

connects the suboccipital plexus and the anterior condylar emissary vein or the internal jugular, if the emissary vein is missing (Ossenberg 1970). Corruccini scored five states for this bridge; 'smooth', 'gutter', 'partial lipping', 'advanced lipping' and 'complete bridge'. This is the scoring method adopted here.

52. Pterygo-basal bridge.
53. Pterygo-spinous bridge.

The pterygo-basal or pterygo-alar bridge connects the inferior surface of the greater wing of the sphenoid to the lateral surface of the lateral pterygoid plate near its root. The trait is age-stable and more common in males (Chouké 1946). The bridge, formed by the ossification of a ligament, usually lies lateral to the f. ovale.

The pterygo-spinous bridge forms by ossification into the pterygo-spinous ligament. This stretches from the middle of the posterior border of the lateral pterygoid plate to, or to some point near, the sphenoid spine. The bridge usually lies medial to the f. ovale, though Wood- Jones noted that it may also pass laterally or even across the lumen. The trait is age-stable (Ossenberg 1970, Chouké 1946) and more common in males (Chouké 1946).

Corrucini noted that both traits are rather rare in their completed form, but partial bridging is common. He scored both traits as 'absent', 'partial in one direction', 'partial in both directions', 'nearly complete' and 'complete'. Ossenberg scored only complete bridging.

54. Spino-basal bridge.

Corruccini described this trait as a bridge, often complete or almost complete, which forms over the foramen spinosum. It was scored similarly to pterygo-basal bridge.

59. Palatine bridge.

These are bridges forming over the lateral palatal sulci, the vascular grooves leading forward from the greater palatine foramen. Bridges over the accessory lateral canaliculi are also included in this trait, which is scored in five states.

Scoring: All bridging traits are scored in 5 states

Bridge absent or partial (states 0-2)	- 0
Bridge almost complete or complete (3-4)	- 1

TUBERCLES AND SPURS.

Tubercles and spurs do not form a homogeneous group with regard to aetiology. Tubercles in general represent intrinsic bony proliferation, similar to that found in exostoses, whereas spurs, like bridging traits, represent an extension of ossification into adjacent structures. Since, however, there still remains much uncertainty as to the origin of some of these traits, they will be grouped together for convenience.

18. Precondylar tubercle.

This is a bony swelling situated several millimetres in front of the anterior margin of the foramen magnum, or on this margin. It is frequently seen on both sides of the median line, separated by a cleft of variable size, and is sometimes continuous with the occipital condyles (Le Double 1903). A single medial tubercle is classed as a bilateral occurrence by Berry and Berry (1967). Median tubercles sometimes develop an articular facet with the atlas. Such a trait has been described as a 'third condyle' and scored as a separate trait, though Oetteking (1930) proposed treating it as a form of precondylar tubercle.

Several theories have been put forward to explain the development of this trait. Kollman (1905) invoked the 'cranial vertebral theory' (that the basioccipital bone is formed by the evolutionary fusion of three or four pre-cervical vertebrae) to explain their presence. He thought that they were the rudiments of the anterior arch of the occipital vertebra. Bolk (1921) cited them as evidence of the positive development potential ('positive Entwicklungskraft') of the medial ends of the occipital condyles. He assumed that normally, the condyles migrate laterally during development, but in some cases the medial ends remain stationary and become tubercles which may fuse.

Charles (1893) thought that tubercles are a response to the strain of carrying heavy loads on the head. He noted that they develop during adult life as ossifications of the suspensory median occipito-atloid ligaments and anterior lateral occipito-atloid ligaments. Bolk (1921) and Oetteking (1930) concur with this view with regard to those tubercles which project from the anterior rim of the foramen magnum into the lumen. Bolk thought these were ossifications of the apicis dentis epistrophei, in connection with the

ligamentum cruciatum atlantis. Finally, Marshall (1955) suggested that tubercles develop in response to the stress of artificial cranial deformation.

Scoring this trait is complicated since, beyond the presence-absence criterion, size, position and structure of the tubercle is very varied. Different forms may also have a different genetic basis. Broman (1957) distinguished between tubercles which were continuous with the condyles (type II) and those which were discrete (type I). He measured the size of the tubercles in male and female American White and Negro crania. Both types showed no significant increase in incidence with age, and no variation in size distribution for either race or sex. The incidence of type I tubercles did not vary with race or sex, but type II was significantly more common in females and in whites, and type II was more commonly bilateral than type I. Broman suggested that type I tubercles represented the ossification of ligaments and type II, developmental anomalies of the kind described by Kollman (1905) and Bolk (1921).

Marshall (1955) employed a "subjective three-point scale evaluation of size" in a large series of crania from Oceania. He found that the tubercles were rarely seen in sub-adults , were 50% more common in males, were frequently larger on the left side of the skull and were associated with general robustness and ruggedness of the skull; the features associated with hyperostotic traits. He suggested that the tubercles are more common and larger in culturally deformed crania. His definition of precondylar tubercle excluded the 'third condyle'.

Scoring: All types of tubercle were included

Tubercle absent	- 0
Small, medium or large tubercle	- 1

36. Trochlear spur.

The trochlear spur is a tiny spine in the roof of the orbit, midway between the supraorbital notch and the lacrimal suture. It is formed by ossification of part of the fibro-cartilaginous trochlea of the superior oblique muscle (Williams and Warwick 1980). Ossenberg found that it achieves expression during adolescence and thereafter remains fairly age stable.

The smoothness of the bony surface in this region enables even tiny protuberances to be noted with little fear of error.

Scoring:	Spur absent	- 0
	Small, medium or large spur	- 1

41. Processus marginalis.

A little below the fronto-malar suture, the posterior border of the malar bone frequently presents a small rounded projection, the marginal tubercle (Williams and Warwick 1980). Czarnetzki (1971) noted that the size of the tubercle was very variable, but scored only absence and presence. In the Greek crania used in this study, some individuals had very large flange-like marginal processes, and a three state scoring system was adopted. A perfectly smooth posterior border (by inspection and palpation) was scored 0, a moderately well defined tubercle, 1, and a large tubercle or flange, 2.

Scoring:	Tubercle absent or small	- 0
	Large tubercle present	- 1

46. Postcondylar tubercle.

Corruccini (1974) described this rare trait as an eminence on the posterior rim of the foramen magnum. These presumably represent ossifications into the posterior atlanto-occipital membrane, which is attached immediately outside the margin of the foramen magnum. Assessment of this trait is more difficult than for precondylar tubercles, since the occipital surface in this region is often irregular. For this reason only medium and large tubercles are scored as present when the trait is dichotomised.

Scoring:	Posterior rim smooth, or small tubercle	- 0
	Well defined medium or large tubercle	- 1

48. Pharyngeal tubercle.

The pharyngeal tubercle is found on the inferior surface of the basioccipital, 10mm. in front of the foramen magnum. It is a small median elevation which gives attachment to the fibrous raphe of the pharynx (Williams and Warwick 1980). Four states were scored for this trait; a perfectly smooth surface was scored 0, a slight eminence, 1, medium and large tubercles were scored 2 and 3. Because this tubercle is not well circumscribed but blends into

the surrounding bone, states 0 and 1 were sometimes difficult to distinguish and were therefore regarded as absent.

Scoring:	Tubercle absent or small	- 0
	Tubercle medium or large	- 1

55. Foramen ovale spine.

A spine may occasionally be seen just inside the f. ovale on the lateral wall, pointing anteriorly or posteriorly. This trait presumably represents ossification into the fibrous tissue surrounding the mandibular nerve and accessory meningeal artery.

Scoring:	Spine absent	- 0
	Spine present	- 1

58. Pterygoid spurs.

These are small spurs on the posterior edge of the lateral pterygoid plate. Corruccini (1974) did not include partial extensions of the pterygo-spinous bridge with spurs, but commented that they may represent related phases of the same trait. They are most easily scored by palpation.

Scoring:	Posterior border smooth	- 0
	One or more spurs present	- 1

EXOSTOSES.

12. Auditory torus.

This is a bony ridge or torus found on the floor of the external auditory meatus. Mann (1984) distinguished two types of torus of different aetiology:

1. *The auditory exostosis*: this occurs in the deep part of the meatus, close to the tympanic annulus. There are usually two smooth surfaced swellings present, anterior and posterior, in the lower half of the meatus. As they increase in size they convert the meatal aperture, normally oval, into an inverted pear-shaped outline. They are almost invariably bilateral. They are caused by chronic or recurrent irritation and there is good evidence that people who habitually swim in cold water are likely to develop them (Belgraver 1935, cited by Mann 1984). Unlike the other tori, the bone

at this site is covered only by very thin skin, with no subcutaneous tissue; it is therefore liable to be affected by changes occuring in the canal. Belgraver demonstrated that, after swimming, the meatus shows a localized hyperaemia in the same area where exostoses develop.

2. *The osteoma*: this occurs in the outer part of the meatus, often solitary and on the posterior wall. Of variable shape (pedunculated, sessile, lobulated or any combination of the three), they occur usually on one side only. Histologically, they have the appearence of osteomas, benign bone tumours most commonly found on the skull. Many tumours are known to have some hereditary basis in their development and, in the absence of evidence that they are caused by any outside influences, these osteomas may be regarded as genetically influenced traits.

Mann goes on to say that most workers who have described auditory torus in populations have failed to distinguish between the deep and the superficial types and, since only the latter could have any genetic basis, the inclusion of auditory torus as a discriminating trait in population studies cannot be recommended. Only Roche (1964) notes the superficial position of the tori described in Australian aboriginal skulls, where he found a very high incidence - 29.7% - mainly in males. In the East African and Mediterranean groups used in this work, the tori noted were of the swimmers' type only; Mann also found no evidence of osteomas in the Egyptian series he examined. It is clear then, that auditory torus must be employed only with great caution as a population discriminator.

Scoring:	Exostosis absent	- 0
	Exostosis present	- 1

23. Palatine Torus.

24. Maxillary Torus.

The torus palatinus is a bony protuberance situated along the midpalatal suture of the hard palate. It is normally bilateral but unilateral ones have been reported. It is formed by the hypertrophy of the spongy and, to some extent, the oral compact bone, the nasal compact layer remaining unaltered. The maxillary torus is a ridge of compact bone occasionally present on the lingual surface of the alveolar border of the maxilla, at the level of the

tooth roots, extending from M3 to P2 and exceptionally as far as the canine. It appears to be limited to adults (Hrdlicka 1940). Similar swellings are more commonly seen on the mandible, and most investigations of these oral tori have focussed on the mandibular and palatine tori rather than the rarer maxillary ones.

As with many non-metric traits, it is difficult to derive an adequately descriptive scale for scoring palatine torus since its form is highly variable. Corruccini (1974) scored a thin sharp ridge as a trace and only a well defined thick exostosis as present. Hooton (1946) described the torus as a ridge (relatively narrow and uniform in width), mound (fairly wide and spindle shaped, the most common form of torus) or lump (having masses of irregular shape, the least common form). Woo (1950) warns that a normal palate may resemble a broad torus if the vascular grooves to either side of it are especially deep: likewise, the depressions in the palatine bones where glandular tissue is lodged may, if particularly well marked, appear to mark the terminations of a low median ridge.

In most ethic groups torus palatinus is found more frequently in females, though Hrdlicka (1940) found a higher incidence in males in some South American groups. The torus appears at an early age; it has been reported in children, the newborn and in one case (Woo 1950) in a fetus. Both size and prevalence increase during the first three decades of life. Palatine and mandibular tori may be correlated. Woo demonstrated a higher incidence of mandibular torus in skulls showing palatine torus, and Suzuki and Sakai (1960) found the two traits to be correlated; other workers (Axelsson and Hedegaard 1985, Kolas et al. 1953, Hrdlicka 1940) found no such correlation in their studies.

The aetiology of these tori is uncertain; some workers view them as functional adaptations to chewing stresses (Hooton 1918, Hrdlicka 1940) while others (Woo 1950, Suzuki and Sakai 1960) favour a genetic cause. Hooton and Hrdlicka both argued that palatine and maxillary tori were the result of chewing stress on the grounds that:

1. They are rarely seen in children.
2. Their incidence increases with age.
3. Their appearance and size is closely related to the degree of tooth attrition.

4. Their incidence is high in groups whose diet contains much raw meat and fish (Lapps, Icelanders and Eskimos).

The work of Suzuki and Sakai (1960), however, suggests that it is genetic factors which determine the presence of the trait. They studied palatine and mandibular torus in Japanese families and found, for both types of torus, that where both parents exhibited the trait, the offspring showed a higher rate of occurence than where one parent only was affected. Incidence of the trait was very low among offspring of unaffected parents. They also found a correlation between the degree of development of the trait in the parents and offspring. Among children exhibiting the tori, in nearly 90% of cases one or both of the parents would also show it.

The aetiology of this feature appears to be highly complex. Lasker (1946) found that Chinese immigrants to America differed from American-born Chinese not only in stature but also in the incidence of torus palatinus. He stressed that physical traits are dependent on both genetic and environmental factors. Axelsson and Hedegaard (1985) cite the work of Dunbar et al. (1968) which showed that in Icelandic skeletal remains, torus palatinus is significantly less common in an edentulous subsample. Axelsson and Hedegaard go on to postulate that, as useless osseous material tends to be resorbed (e.g. the alveolar borders following tooth loss) Dunbar's finding suggests that torus palatinus is partly the result of an increased demand on the masticatory system. Also, the strength of the jaw muscles decreases after the age of thirty (Franks and Hedegaard 1973) and this could lead to resorption and account for the decreased incidence of palatine torus after the third decade of life (Kolas et al. 1953).

Scoring:	Torus absent or trace only	- 0
	Large well-defined torus	- 1

For palatine torus, thin sharp ridges or small, low, poorly defined swellings were scored as traces. For maxillary torus, small irregularities near the molar alveolar margins were also scored as traces.

4. Foraminal Traits.

Foraminal traits are those relating to the passage of nerves and vessels through bony structures. The traits record the absence, number and position of foramina. The variation shown by foraminal traits has several possible developmental sources:

> Not only are variations in the presence or absence and degree of branching of a nerve or blood vessel involved, but also the relative position of the bone with respect to the nodes of the branches. . . It is also possible that the degree of branching . . . may be especially susceptible to environmental influences.
>
> (Cheverud and Buikstra 1981)

Foraminal traits are grouped, for convenience, into five categories; vascular, emissary, sutural, accessory and variable foramina.

VASCULAR FORAMINA:

34. Nasal foramen

EMISSARY FORAMINA:

4. Parietal foramen
15. Mastoid foramen absent
16. Postcondylar canal patent
51. Foramen of Vesalius

SUTURAL FORAMINA:

14. Mastoid foramen exsutural
28. Anterior ethmoid foramen exsutural

ACCESSORY FORAMINA:

22. Accessory lesser palatine foramina
30. Accessory infraorbital foramen
56. Accessory foramen spinosum
60. Zygomatico-facial foramen multiple

VARIABLE FORAMINA:

25. Zygomatico-facial foramen absent
29. Posterior ethmoid foramen absent
42. Zygomatico-temporal foramen
43. Zygomatico-orbital foramen

VASCULAR FORAMINA.

Vascular foramina transmit small veins only. The emissary foramina come into this category but, since they specifically connect with the intracranial sinuses, they are grouped under their own heading.

34. Nasal foramen.

The external surface of the nasal bone is frequently perforated near its centre by a foramen for the transmission of a small vein (Williams and Warwick 1980). Perizonius suggests that this may be used as a non-metric trait. Since nutrient foramina are commonly found in this area, only well defined foramina, and not pin-holes, are scored.

Scoring:	Foramen absent	- 0
	Foramen present	- 1

EMISSARY FORAMINA.

Emissary foramina transmit small veins which connect the intracranial sinuses with the extracranial venous system. Ossenberg found that their incidence was greater in culturally deformed crania. She postulated that this reflects an attempt to establish alternative routes of circulation to "compensate for constriction deep in the bindings". It may also be interpreted as evidence for a common aetiological factor in these traits, though Ossenberg found no correlation in pairs of emissaria.

4. Parietal foramen.

This pierces the parietal bone near the sagittal suture a few centimetres in front of lambda. It transmits a vein draining the superior sagittal sinus and sometimes a small branch of the occipital artery (Berry and Berry 1967). A single median foramen sometimes occurs and rarely, the opening is abnormally large. Boyd (1930) found unilateral expression to be commoner on the right side than the left. Ossenberg also found this trait more commonly on the right, and the incidence was higher in males. She noted a slight increase in incidence with age. Corruccini scored the trait as partially complete when external foramina were visible but failed to pierce the inner table of bone.

Scoring:	Foramen partial or absent	- 0
	Foramen present	- 1

15. Mastoid foramen absent.

The mastoid foramen normally lies on or near the suture between the mastoid part of the temporal bone and the occipital bone (Berry and Berry 1967). The canal is often long and

tortuous so that it is impossible to pass a probe, which leads to doubt as to whether an emissary foramen or a blind canal is present (Boyd 1930). The trait was scored as present only if a wire could be passed through the canal into the sigmoid sinus (detected by palpation in complete specimens). The foramen may be multiple. In some of the crania from Sedment, an interesting variant was noted. A canal piercing the sigmoid sinus was present, but it emerged on or near the suture between the mastoid and the parietal bone, near the parietal notch. This trait was not scored as a true mastoid foramen in this study.

Scoring:	Foramen absent or blind ending	- 0
	Patent canal present	- 1

16. Postcondylar canal patent.

This canal pierces the condylar fossa which lies immediately posterior to the occipital condyle. It sometimes ends blindly and is only scored as patent when a probe can be passed through it. In poorly preserved specimens the fragile bone of the fossa may be broken, making scoring unsatisfactory (Berry and Berry 1967). Corruccini (1974) scored partial canals as 'intermediate' and noted that the fossa and its perforation are apparently independent traits. Boyd (1930) and Ossenberg (1970) found the trait more commonly on the right side. Ossenberg noted a preference for females and an irregular age pattern, incidence decreasing between childhood and adolescence, but increasing thereafter.

Scoring:	Fossa absent or present	- 0
	Canal piercing fossa	- 1

51. Foramen of Vesalius.

This, the least common of the emissary foramina, is situated anteromedial to the f. ovale. It carries venules draining the cavernous sinus which normally pass through the f. ovale. Ossenberg (1970) found an inconsistent age pattern with decreasing incidence between childhood and adolescence and an increase in adulthood. She found no sex difference, but the trait was more common on the left side. Partial foramina, through which a probe could not be passed, were classed 'intermediate' by Corruccini (1974).

Scoring:	Foramen absent or intermediate	- 0
	Foramen present	- 1

SUTURAL FORAMINA.

These traits refer to the position of foramina which develop within sutures, but may become enveloped by adjacent bones.

14. Mastoid foramen exsutural.

The mastoid foramen, normally lying on the occipito-mastoid suture, may pierce the mastoid bone or, more rarely, the occipital (Berry and Berry 1967). When multiple foramina were present, the trait was classed as absent if any foramen lay on the suture (Corruccini 1974). When calculating the incidence of this trait, the denominator should be based on the number of skulls in which the foramen is present, not the total sample size which Berry and Berry used in their original paper, though they corrected this error in later papers.

28. Anterior ethmoid foramen exsutural.

The anterior ethmoid foramen usually lies on the suture between the orbital plates of the frontal and ethmoid bones. It transmits vessels and nerves of the same name from the anterior cranial fossa. The foramen develops in the suture line but may become enveloped by the frontal bone (Anderson 1983). Corruccini points out that the trait may be difficult to classify when the lacrimal suture dips into the rim of the foramen but may or may not enter it sufficiently , and when the suture is obliterated. The trait may also be multiple.

Scoring:	For both traits:	Foramen lying in the suture	- 0
		Foramen exsutural	- 1

ACCESSORY FORAMINA.

These traits represent both the branching of nerves which are usually single, and the formation of bone around the branches.

22. Accessory lesser palatine foramina.

These foramina lie on both sides of the posterior border of the hard palate, immediately posterior to the greater palatine foramen, and transmit the lesser palatine nerves. When more than one foramen is present it is scored as accessory by Berry and Berry. Perizonius

warns that confusion may be caused by cracks and fissures, or by accessory greater palatine foramina. Corruccini notes that these foramina often occur in the valley posterior to the tuberosity of the third molar, where they are difficult to observe.

30. Accessory infraorbital foramen.

This varies from a small slit on the border of the infraorbital foramen to a large, separate foramen. Perizonius scored only those openings which were connected with the infraorbital canal as present, since pits and nutrient foramina abound in this region.

56. Accessory foramen spinosum.

The foramen spinosum may occasionally be multiple. This trait may include the canaliculus innominatus, a tiny canal on the medial side of the f. spinosum, transmitting the lesser petrosal nerve which usually passes through the f. ovale (Anderson 1983).

60. Zygomatico-facial foramen multiple.

The zygomatico-facial foramen, transmitting nerves and vessels of the same name, may be single or multiple. Corruccini scores only "true foramina, not pinholes, . . . but this distinction is often arbitrary". Since this foramen is sometimes absent (forming the basis of another trait), the incidence of multiple zygomatico-facial foramen should be based on the number of skulls in which the foramen is present, rather than the total sample. Absence of the foramen relates to absence of the nerve, while accessory foramina relate to nerve branching and ossification around the branches. Deriving the incidence as stated above therefore gives the trait more 'biological meaning' and overcomes the problem of correlation between the two traits, certain expressions of which are mutually exclusive.

Scoring: For all accessory foraminal traits:

One foramen only present	- 0
Two or more foramina present	- 1

<u>VARIABLE FORAMINA.</u>

The term 'variable foramen' refers to the fact that the nerves which pass through them may occasionally be absent, in which case the foramen does not form. Vessels often

accompany the nerves, but ontogenists have long regarded nerves as being more developmentally stable than vessels, therefore this category relates only to foramina which transmit nerves.

25. *Zygomatico-facial foramen absent.*
42. *Zygomatico-temporal foramen.*
43. *Zygomatico-orbital foramen.*

These three foramina transmit branches derived from the zygomatic nerve. This nerve, a branch of maxillary V, traverses the pterygo-palatine fossa and enters the orbit via the inferior orbital fissure. It courses along the lateral wall of the orbit, then splits into two branches, the zygomatico-facial and zygomatico-temporal nerves. They enter the zygomatico-orbital foramina (two are usually present) which lie on the infero-lateral surface of the orbit, near the rim. Two canals lead from these foramina; one emerges on the temporal surface of the zygomatic bone, near the base of the frontal process, as the zygomatico-temporal foramen, the other as the zygomatico-facial foramen on the anterior surface of the zygomatic bone (Williams and Warwick 1980).

One or both of these nerves and their associated canals may be absent. Clearly, absence of the zygomatico-orbital foramina implies absence of the other two, though both canals may diverge from a single orbital foramen. For this reason it is not clear whether zygomatico-orbital foramen constitutes a useful trait if the other two are also recorded, though Perizonius uses all three. They may also be confused with nutrient foramina, especially on the temporal surface of the zygomatic bone. For this reason only well defined foramina and not 'pin-holes' are recorded. *Absence* of the zygomatico-facial foramen is scored positive by Berry and Berry and other workers, while Perizonius scores *presence* of the other two traits as positive. Following the recommendation of Corruccini, the observed number of zygomatico-facial foramina is recorded, though only presence and absence is recorded for the others.

Scoring: For zygomatico-facial foramen:

One or more foramina present	- 0
Foramen absent	- 1

For zygomatico-temporal and -orbital foramen:

Foramen absent	- 0
One or more foramina present	- 1

29. Posterior ethmoid foramen absent.

This foramen, like the anterior ethmoid foramen, lies on the fronto-ethmoid suture. Corruccini notes that it is rarely absent, and Berry and Berry caution that this trait is particularly difficult to score in poorly preserved specimens.

Scoring:	Foramen present	- 0
	Foramen absent	- 1

5. Miscellaneous traits.

The twelve remaining traits will now be described. These are:

1. Highest nuchal line
9. Fronto-temporal articulation
17. Bifaceted condyles
19. Hypoglossal canal bridge
26. Supraorbital foramen complete
27. Frontal notch or foramen
33. Nasal sill sharp
37. Trochlear fossa
38. Frontal grooves
40. Os Japonicum trace
47. Jugular foramen bridge
49. Pharyngeal fossa

1. Highest nuchal line.

The highest nuchal line (linea nuchae suprema), a faintly marked, often almost imperceptible line, is the site of insertion of the occipitalis muscle and the epicranial aponeurosis. Corruccini classified this as an 'anthroposcopic' trait (namely, one which is not discrete such as the brow ridge or parietal bossing), and eliminated it from his study. Merkel (1871, cited by Corruccini) showed that this feature was highly variable and that its expression was dependant on the form of the superior nuchal line.

Scoring:	Line absent	- 0
	Line present	- 1

This trait was scored by visual inspection, though other workers have scored it by palpation (A. C. Berry, personal communication).

9. Fronto-temporal articulation.

The type of pterion is determined by the relative growth of the four bones which meet in this region. Kokott (1933) postulated that mechanical factors determine the eventual configuration of the pterion. He regarded the sutures in this region as indicating lines of condensation in the dura mater which, at an earlier stage, control the growth of the membranous capsule. These condensations act as bracing ropes anchoring the membranous

vault to the phylogenetically older base; the strips are non-osseous and later on, bone does not grow over them (Moss 1954). Murphy (1956), however, found no significant correlation of pterion configuration with cranial index, post-orbital breadth or basi-cranial angle and concluded that genetic factors must also be considered in the aetiology of this trait.

Scoring:	No fronto-temporal contact	- 0
	Fronto-temporal contact	- 1

Corruccini scored stellate contact as intermediate, but in this study any degree of fronto-temporal contact is scored as present.

17. Bifaceted condyles.

Occasionally the occipital condyle has two articular facets. Corruccini noted that, although the endpoints are clearly defined, the trait is actually continuous in nature, various degrees of constriction or notching being observed. The trait is scored in five states, from single condyle (0), notches on one (1) or both (2) sides, almost divided facet (3) to two distinct facets (4).

Scoring:	Condyle single or notched (0-2)	- 0
	Condyle almost or completely double (3-4)	- 1

19. Hypoglossal canal bridge.

The hypoglossal canal, which transmits a meningeal branch of the ascending pharyngeal artery as well as the hypoglossal nerve, may be partially or completely divided into two by a spicule of bone. The hypoglossal nerve emerges from the brain as 10-15 rootlets. They are collected into two rootlets which perforate the dura mater separately opposite the hypoglossal canal. Each fascicle acquires a separate dural sheath and after passing through the canal the fascicles unite.

Divisions of the canal (by connective tissue or bone) has been interpreted as giving support to the vertebral theory of the basioccipital bone (O'Rahilly and Müller 1984), the canal itself reflecting amalgamation of the intervertebral foramina. Dodo (1980, cited by Dodo 1986) noted the presence of hypoglossal bridging in fetal skulls, suggesting that genetic factors predominate in the expression of this trait.

Ossenberg classed hypoglossal canal bridging as a hyperostotic trait, the incidence of which increases slightly with age. However, the observation of Dodo (1980) that almost all cases of bridging are already established by the end of fetal development suggests that their aetiology differs from the hyperostotic bridging traits described earlier, which are mainly age progressive. Hauser and De Stefano (1985) found no significant side difference, but there was a slight tendency for unbridged canals to be expressed more frequently on the right, and bridged ones on the left in Europeans (the side distribution associated with hyperostotic traits). Dodo (1980) found neither sex nor side differences in the Japanese crania he examined.

Corruccini observed a complete range of variation in this trait between absence, unconnected spicules and complete bipartition of the canal. Hence the trait was scored in five states relating to the degree of bipartition.

Scoring:	Canal single or partially bridged (0-3)	- 0
	Complete bridge present (4)	- 1

26. Supraorbital foramen complete.
27. Frontal notch or foramen.

Much confusion surrounds the definition of these two traits. Both are found at the upper rim of the orbit, as shallow or deep notches or as foramina. They mark the path of nerves and vessels originating deep in the orbit which cross the orbital rim onto the frontal bone.

Gray's Anatomy (Williams and Warwick 1980) gives the following account of these traits:

> The lateral two-thirds of each supra-orbital margin are sharp; the medial one-third is rounded. At the junction of these two parts is the supraorbital notch, which may on occasion be a foramen, and contains the supraorbital vessels and nerve. *Medial* to this notch the small frontal notch or foramen is present in about 50 per cent of skulls. Both features show a sexual dimorphism (my emphasis).

This description of the frontal foramen contradicts that of Berry and Berry and of Corrucini who maintain that the frontal foramen lies *lateral* to the supraorbital foramen. Ossenberg describes a 'supratrochlear foramen', carrying the supratrochlear vessels and nerves, which appears to be synonymous with the frontal foramen of Williams and Warwick. In the following discussion the term 'frontal foramen' will therefore refer to a laterally placed foramen.

Jantz (1970, cited by Corruccini) notes the difficulty of distinguishing between a "laterally occurring supraorbital foramen, or a medially occuring frontal foramen". Corrucini acknowledges this, but maintains that:

> the frontal foramen can be distinguished by its inclination towards the back of the orbit and by the depth of bone around it when it penetrates; the supraorbital foramen seems always to just barely pierce the margin and is surrounded at most by a thin ring of bone.

He scored any foramen from the lateral half of the supra-orbital margin to approximately halfway back to the coronal suture as a frontal foramen, and a foramen which failed to connect with the orbit as intermediate. Corruccini's criteria have been adopted in this study; in addition, a notch on the lateral border has also been scored as a frontal foramen (Berry and Berry 1967).

Ossenberg explained the presence of supraorbital notches as the result of differential growth between the orbital margin and the nerves and vessels crossing it. Where the latter cannot keep pace with growth of the bone, they are encroached upon and eventually surrounded by bone. She found that the supraorbital foramen was more common in males and on the left, a feature of hyperostotic traits, and that it was age progressive until adulthood and relatively stable thereafter. Korey (1980) also found this trait to be age progressive, even in adult crania. Hence, there is some justification for regarding these traits as hyper-ostotic, but only in the relative sense .

The identity of the nerves and vessels which pass through the frontal foramen is unclear. The frontal nerve (a branch of ophthalmic V) runs along the roof of the orbit, dividing halfway along into a small supratrochlear and a large supraorbital branch. The supratrochlear branch passes above the trochlea and emerges at the antero-medial rim to innervate the skin of the glabellar region of the forehead, the upper eyelid and conjunctiva. The supraorbital branch ascends the forehead with the supraorbital artery before branching into a lateral and smaller medial nerve which innervate the scalp (Williams and Warwick 1980). It is conceivable that the frontal foramen carries a prematurely arising lateral supraorbital nerve, or it could represent a lateral migration of the supraorbital foramen. In the latter case, the supra-trochlear foramen may be mistaken for

the supraorbital, though the author has encountered skulls in which all three notches are present.

Kimura (1977) suggested a new method of scoring to overcome these difficulties. He devised three categories:

1 Supraorbital foramen present.

2. Supraorbital sulcus present.

3. Supraorbital foramen and sulcus present.

Perizonius adopted this method, but since it still fails to discriminate between laterally and medially placed notches, and does not provide a comprehensive description of variation in this region, it has not been adopted here.

Corruccini points out that the supraorbital foramen shows continuous rather than discrete variation. Five states have been scored here; absence of a notch (0), shallow notch without spicules (1), deep notch with one or two spicules (2), almost complete foramen (3) and complete foramen (4).

Scoring: For supraorbital foramen:

Complete foramen absent (0-3)	- 0
Complete foramen present (4)	- 1

For frontal foramen:

Foramen absent or intermediate	- 0
Complete foramen or notch present	- 1

33. Nasal sill sharp.

The inferior narial aperture may be bounded by a sharp margin separating the floor of the narial cavity from the superior alveolar surface. This sharp ridge may, or may not, culminate in the development of a prominent nasal spine. Alternatively, the margin may be smooth and rounded, usually without a nasal spine (Wood-Jones 1931a). Corruccini scores this trait as a midline one, but in this study the left and right margins are scored separately.

Scoring:

Nasal sill rounded	- 0
Nasal sill sharp	- 1

37. Trochlear fossa.

This trait has not been used in previous studies. Williams and Warwick (1980) note that:

> near the junction of the (orbital) roof and medial wall, and close to the orbital opening, the small trochlear fossa (occasionally replaced by a trochlear spine) marks the attachment for the fibrous loop for the tendon of the superior oblique muscle of the eyeball.

They imply that either a fossa or a spur is present, but Le Double (1903) states that the trochlear fossa is often surmounted by a spur. Similarly, in the series examined here it was noted that a small rounded depression, located anterior and inferior to the trochlear spur, frequently occurred. It was therefore scored as a separate trait. It was scored in four states; depression absent (0), slight depression (1), medium (2) and deep depression (3).

Scoring:	Fossa absent or slight	- 0
	Fossa medium or deep	- 1

38. Frontal grooves.

Dixon (1904) described grooves on the frontal bone which indicate the position of one or more branches of the supraorbital nerve. He attributed their origin to "a want of agreement between the rate of growth in length of the overlying nerves and rate of expansion of the cranium". The grooves may be shallow and faint or deeply cut and strongly marked, sometimes forming short tunnels within the frontal bone.

Dixon studied the incidence of frontal grooves in several populations and found:

1. Where the incidence is high, bilateral presence and strong marking is more common.
2. In populations with a low incidence of grooves, bilateral presence is rarely seen.
3. Where grooves are present on one side only, they are more commonly found on the left.
4. The presence of grooves was not related to the supra-orbital notch or foramen, or to metopism.

Ossenberg found this trait to be relatively age stable and slightly more common in males and on the left. She also noted a low positive correlation between this trait and supra-orbital foramen, in contrast to the findings of Dixon. This trait may be regarded therefore as hyperostotic, but only in the relative sense.

Scoring:	Frontal grooves absent	- 0
	Frontal grooves present	- 1

40. Os Japonicum trace.

This is described by Ossenberg as a posterior trace, 2-10 mm. long, of the anomalous transverso-zygomatic suture which, if complete, divides the malar into two parts. In contrast to the extremely rare os Japonicum, this suture is fairly common in many populations. Ossenberg found that this trait showed a tendency to decrease with age. She defined this trait as a hypostotic sutural variation but, since development of the transverse suture implies the presence of an accessory centre of ossification in the malar bone, this trait's aetiology may involve more than a simple retention of infantile characters. It is therefore grouped separately from metopism and infraorbital suture.

Scoring:	Suture trace absent	- 0
	Suture trace present	- 1

In one skull (from Giza) a full os japonicum was seen. This was scored as a positive trace, since the full os Japonicum was not recorded in this study.

47. Jugular foramen bridge.

This is another trait where confusion over definition is found. Corruccini takes it to mean a superiorly placed spur dividing the jugular fossa, though he mentions a second medial type of bridging. Dodo (1986), however, defines the bridge as a process extending anterolaterally from the jugular notch of the occipital bone (just anterior to the hypoglossal canal) to the jugular fossa of the temporal bone, *posterior* to the triangular depression of the petrous temporal. A process may also extend from the temporal to the occipital, and frequently two processes occur which make contact, though a suture-like gap is always present. These bridges he denotes as type I bridges.

Dodo also describes bridges where this intrajugular process extends anterior to the triangular process (which he does not regard as a true bridge). These types of bridge are found in fetal and adult skulls. Another type is found in adult skulls (type II bridges) where a bony process arises posterior to the hypoglossal canal and extends to the intra-jugular process of the temporal bone, thus dividing the fossa in two halves. Again, no bony fusion occurs; a suture-like gap separates the processes. This type of bridge probably develops along the dural sheath between the vagus and accessory nerve (Dodo 1986), and may

perhaps be regarded as a hyperostotic bridging trait, though its rarity could account for the failure to observe it in fetal crania.

Unfortunately, this trait cannot be used to discriminate between the Greek and Egyptian crania used in this study since the Greek groups were scored in 1985 according to Corruccini's criterion, and the method of scoring was revised following the publication of Dodo's paper. Dodo combined type I and II bridges in his analyses, and this method was followed for the Egyptian and Kenyan crania, though a case could be made for regarding the two types as separate traits since both types may occur in the same fossa.

Jugular foramen bridge is not classed here with the hyperostotic bridging traits since, like the hypoglossal canal bridge, the trait makes its appearance during the fetal period (Dodo 1986). As with other bridges, five states were scored, though the complete bridge always showed a suture-like gap.

Scoring:	Bridge absent or partial (0-2)	- 0
	Bridge almost or fully formed (3-4)	- 1

49. Pharyngeal fossa.

The pharyngeal fossa (fovea bursae or medio-basal fossa) is a small oval depression in the inferior surface of the basioccipital, anterior to the sit of the pharyngeal tubercle. It varies in depth from 2 to 7 mm., its width is approximately 4 mm. wide and its length, 5 - 11 mm. (Sullivan 1920). Corruccini notes that there is a continuous gradation between a flat pars basilaris, a shallow depression and a well formed fossa as described by Sullivan. The aetiology of this feature is unclear. Romiti (1891, cited by Sullivan 1920) claims it is produced by a pharyngeal diverticulum, either normal or accessory. Perna (1906) thought it marks the site of the canal left by the notochord (vertebral theory of the cranium).

Sullivan showed this to be a rare trait, though some New World groups show an incidence up to 25%. Since the high frequency groups coincide with those grouped together on a linguistic basis, Sullivan concludes that the pharyngeal fossa is "transmitted by inheritance".

Scoring:	Fossa absent or slight (0-1)	- 0
	Fossa medium or deep (2-3)	- 1

4.3. Methods: Analytical procedures.

The analytical procedures take the following form:

i) A preliminary analysis of the data is undertaken for both the metric and the non-metric traits.

ii) The distance measures are generated for both the metric (Mahalanobis D^2) and non-metric (Grewal-Smith MMD with the Freeman-Tukey transformation) traits.

iii) Multi-dimensional scaling (MINISSA) methods are used to generate co-ordinate points for the groups in three-dimensions. These points are then plotted to enable visual inspection and assessment of the distances.

iv) Comparisons of the different plots (e.g. metric vs. non-metric, male vs. female) are finally undertaken. The method employed is Procrustes analysis (Gower 1971), using the GENSTAT 'ROTATE' directive.

4.3.1. Preliminary analysis of the data.

4.3.1.1. Metric traits - basic statistics and one-way analysis of variance.

Before embarking on a complex multivariate analysis the data should be examined with standard univariate statistical methods. Examination of the ranges, means and standard deviations will often unearth errors in the data which would otherwise be missed. Univariate statistics are generated using the GENSTAT 'BASIC' subroutine. As well as the standard statistics, this package calculates the coefficients of skewness and kurtosis, which can be used to test for normality (Pearson and Hartley 1958).

One-way analysis of variance is also carried out on each of the 10 variables (using the MINITAB package) to show whether the variables taken individually are capable of distinguishing between the thirteen groups. The MINITAB analysis of variance program also generates a plot of the group means with 95% confidence intervals.

Tests of homogeneity are also carried out on the dispersion matrices of several data sets using a specially modified version of the GENSTAT subroutine 'CVAID' into which are incorporated Box's (1949) homogeneity tests. Since the latter require complete data sets, only the 5 most common variables (GOL, XCB, NPH, OBH, NLB) are analysed, thus

maximising the number of useable skulls in each group. It is not possible to include the two Cretan samples in these analyses since they are too small.

4.3.1.2. Non-metric traits - 'Generalised Linear Interactive Modelling ' procedures.

Of the 13 groups studied here, the 5 Greek and 2 Cretan samples are excluded from the preliminary analyses on the grounds of poor condition and small sample size. Preliminary analysis of the raw data is undertaken with the following aims:

a) Since there is no consensus as to the best method of determining the incidence of bilateral traits, study of the patterns of association between trait expression and side may aid in determining which method to use.

b) Certain traits may best be excluded from the study by reason of their correlation with other traits, or because the trait expression is sex-related in an analysis where the sexes are pooled.

c) The error incurred in the scoring of some traits may be unacceptably high. Such traits should be identified and discarded from further analysis.

The first two aims, and to some extent the third, may be achieved by the use of a single computer package, GLIM (Generalised Linear Interactive Modelling, Baker and Nelder, Rothamstead Experimental Station). Using GLIM, data in the form of contingency tables may be examined to reveal patterns of association. The GLIM program employs *generalised linear models*, a theoretical account of which may be found in Dobson (1983), McCullagh and Nelder (1983) and Baker and Nelder (1978). Appendix 3 contains a brief description of these models andexamples of output from a GLIM modelling session.

The preliminary analysis of the data is in three parts:

I. All 60 non-metric traits are individually examined using the GLIM package to determine whether trait expression is affected by sex or population and, in the case of bilateral traits, to look for differences or associations between the left and right sides.

II. Selected pairs of traits are examined for correlation using Chi-square tests and GLIM.

III. A sample of 40 crania, examined on two occasions, is used to assess the magnitude of intra-worker error in the scoring of traits, with the aim of excluding 'difficult' traits from further analysis. Inter-worker error is also briefly examined for 30 of the 60 traits.

4.3.1.2.1. Trait expression: sex, side and population effects.

A. MODELLING PROCEDURE.

For each bilateral variant a four-way contingency table is constructed, the four margins of the table (or *factors*) being population (6 groups or *levels*), sex (2 levels), left expression (2 levels, absent and present) and right expression. The table has 6x2x2x2=48 cells and each cell contains the *count*, or number of skulls in that category. The 48 values are entered as data into the GLIM program, along with an indication of which value represents which cell of the table.

Underlying the use of modelling methods is the concept that the observed data (the counts) can be reproduced by a model containing a set of explanatory factors (i.e. the population, side and sex) and their associated parameters. These parameters determine the magnitude of the factor effects, or the extent to which each factor contributes to the value that the model predicts for the cells of the table (the *fitted values*). The factors on which the model is based are decided by the experimenter but the parameter values are unknown. The GLIM program calculates maximum likelihood estimates of the parameter values.

For each table of counts, a succession of models is generated, each based on a different set of factors or *terms*. The models are not limited to single factor effects alone, but can include terms representing the interaction of factors. After each model has been generated, and its parameters estimated, the fitted values produced by the model are compared to the original values. A null hypothesis is proposed, that the fitted values represent the values in the population, while the observed values are the values in a sample from that population. If the distribution and size of the discrepancies is consistent with that arising from sampling error, the null hypothesis is accepted. Otherwise the model is rejected as

poorly fitting, and other models are investigated until one that adequately fits the data is found.

The model is tested for goodness-of-fit to the original data by a log-likelihood ratio test and the resulting statistic, the *deviance* and its degrees of freedom, are printed. This deviance is equivalent to the amount of the variance in the data attributable to sampling error. The log-likelihood distribution approximates the Chi-square distribution, so that Chi-square tables may be used to determine if this value, the 'residual' deviance, is significant. If the deviance is not significant at the 5% level, the model is regarded as adequate.

It will be realised that the number of models which could be investigated is vast. For a four-way table there are 15 different terms, any number or combination of which could theoretically form the basis of a model. Also, several of the possible models may adequately fit the data. In practice, there are rules and constraints governing the procedure of model fitting, and the principle of parsimony dictates that the simplest model which adequately fits the data is preferred to more complex ones. The modelling procedure will now be described.

1. The null model.

This is the first model fitted. No factor terms are included and the fitted value, which is the same for each cell, is the mean count (total number of skulls divided by the number of cells). All the variation in the data is thus attributed to sampling error.

2. The minimum model.

The null model is the simplest model but in most cases it will not adequately represent the structure of the data. The second model to be fitted is the minimum model, containing those factors which must be included in any model, such as the fixed marginal totals of the contingency table. These factors are:

p - the population factor. This factor has six levels, one for each of the six populations in the analysis. It is necessary since each group contains a different number of skulls and this will affect the values predicted in the cells for each of the groups.

x - the sex factor. The number of males and females in the analysis will also affect the predicted values.

p.x - the population-sex interaction factor.

The two single factors 'p' and 'x', the *explanatory variables*, represent the fixed marginal totals i.e. fixed in the sense that the sex distribution and number of skulls in each group are of no biological significance. It is further known that the sex ratio is different in each group, necessitating a term in the model to account for this source of variation in the data. This is the *two-factor interaction* term 'p.x'.

Two more terms are included in the minimum model. They are the *response variables*, which are:

l - the left expression factor.

r - the right expression factor.

Although these two factors are of biological significance, the only information they contain is about whether trait presence or absence is more common. The purpose of this modelling is to test for the interaction of trait expression with sex, side and population. To do this, models containing two-factor interaction terms relating to 'l' and 'r' must be studied. It is a general rule of modelling that interaction terms can only be included when the individual single factors are already present, so the factors 'l' and 'r' are placed in the minimum model. The minimum model for a bilateral trait consists of the following terms:

$$p + x + l + r + p.x.$$

3. Two-factor interactions.

The minimum model may provide a sufficiently good fit for some traits, especially the rarer ones where low counts in most of the cells mean that there is insufficient data to test for more complex interactions. Where the deviance after fitting the minimum model is significantly large, the five remaining two-factor terms (p.l, p.r, x.l, x.r and l.r) must be tested. Note that all of these terms include either the factor 'l' or 'r', and relate to the sex, side and population effects on the trait expression. The two factor term 'p.x' has already

been included in the minimum model since it represents a known effect, whereas the effects of the remaining terms are hypothetical.

The significance of an interaction is determined by fitting two models whose terms are identical except that one of them excludes the term under investigation. The difference in the deviance of the two models (for the difference in the degrees of freedom) reveals whether that term has a significant effect in the model.

The significance of a term, however, depends on what terms are already in the model. The testing of terms may be approached in two different ways:

a. Each two-factor term alone may be added in turn to the minimum model. However, with this method it is possible to overestimate the significance of the terms. For example, 'p.l' and 'p.r' may both be significant, but if the left and right expressions are highly correlated (i.e. 'l.r' is highly significant), one of the two expressions in the model may be redundant.

b. An alternative method adds all remaining two-factor terms to the minimum model, then each is excluded in turn, putting the excluded term back into the model before testing the next one. This method, however, may fail to distinguish a significant term. For example, 'p.l' may not be significant if its effects are masked by the presence of 'p.r' and 'l.r' in the model. If 'p.r' is also insignificant for the same reason, it might be falsely concluded that no population effects were present in the data.

Of the two methods, the second one is prefered here on the grounds that, although it may fail to detect some associations, those that it does detect are certain. The problem of failing to detect significant terms may be partly overcome by excluding all non-significant terms from the model (apart from those in the minimum model) and examining the fit of the final model. If the fit is inadequate, this implies that one of the excluded terms may be required after all. In this case, the least non-significant term could be added, and the new model's fit assessed. Alternatively, both methods could be used, but this is cumbersome and unnecessary as in most cases, the final model containing only the significant terms is found to be adequate.

A significant value for the terms 'x.l' and/or 'x.r' indicates that the expression of the trait varies with the sex. If 'p.l' or 'p.r' are significant, that trait will discriminate between populations. The term 'l.r' indicates association between the expressions on the left and right sides.

4. Three-factor interactions.

Occasionally, the model containing all one and two- factor terms will have a deviance sufficiently high to indicate that other more complex terms are needed to sufficiently describe the patterns in the data. These are the three-factor interactions, 'p.x.l', 'p.x.r', 'p.l.r' and 'x.l.r'. If three-factor terms are implied, the testing procedure is as follows.

A model is fitted consisting of all the one, two and three-factor terms, and its scaled deviance is noted. Each of the three-factor terms is then tested for significance by fitting models which exclude them. Once the significant three-factor terms have been identified, the two-factor terms can be tested. It has been noted earlier that more complex terms should not be included unless the simpler terms which they contain are already in the model. Thus, a significant three-factor term contains three two-factor terms which are a necessary part of the model e.g. if the term 'p.x.l' alone is significant, then the terms 'p.x', 'p.l' and 'x.l' must be included, but the terms 'p.r', 'x.r' and 'l.r' may be tested. When all the significant terms have been identified, the final model can be generated.

Significant three-factor interactions may be interpreted in two ways. It could be concluded that some complex biological mechanism is involved in the expression of that particular trait (e.g. a significant 'p.x.l' term might suggest that the sex effect on a trait varies in different populations, possibly due to environmental effects). Alternatively, errors in scoring the trait may be obscuring simpler biological principles, and such a trait might be expected to show high inter- and intra-worker scoring errors. In either case, traits showing significant three-factor interactions are best excluded from further study.

5. The four factor interaction.

The four-factor term 'p.x.l.r' can only be added to the model when all the smaller terms which it contains are present. Such a model is called the *full model*, and it reproduces the original data exactly, but without any simplification of the data.

Use of GLMs in testing midline traits.

For midline traits, the same procedure is followed as for bilateral traits, though the following points should be noted:

a. The contingency table is three-dimensional and the factors 'l' and 'r' are replaced by the single factor 't', the trait expression.

b. The minimum model is of the form p + x + t + p.x.

c. The only testable factor interactions are 'p.t', the effect of group on trait expression, and 'x.t', the sex effect.

Example Program 1 in appendix 3 demonstrates modelling of a midline trait (for 2 groups only). This example is designed as an aid to understanding GLMs; it does not represent good modelling practice. Example programs 2 and 3 illustrate the modelling procedure used in this study for traits showing evidence of two- and three-factor interactions respectively.

B . INTERPRETATION OF THE GLM.

There are two aspects of the output of the GLIM program which require interpretation. These are:

1. The deviance used to asses the goodness of fit of the model, and

2. The parameters associated with the terms in the model.

Not infrequently, inconsistencies may arise when a large number of data sets are being tested, and some guiding principles for dealing with them will be mentioned.

1. The deviance.

Two types of deviance may be noted:

a) The deviance associated with a particular model, and

b) The deviance associated with a particular term, being the difference in the deviance of two models which differ by a single extra term.

The deviance for the model is a log-likelihood ratio statistic, and its distribution approximates the Chi-square distribution, though little is known about the closeness of the approximation. It might at first seem that the smaller the deviance, the better the model but the closeness of fit depends largely on the number of factor terms included. The full model provides a perfect fit, but it has so many parameters that there is no simplification

of the data. The 'best' model, then, is the simplest one whose deviance is acceptable (i.e. not significant) and 'over-fitted' models (whose deviances are very small), should be viewed with suspicion and simpler models sought. If the deviance of a model is just significant, it may be better to accept that model since the Chi-square values are only approximate, than to fit more complex terms.

The Chi-square approximation to the deviance associated with a term is thought (Baker and Nelder 1978) to be a better approximation than that to a model's deviance. However, a just significant term may be excluded from a model if it leads to overfitting; likewise a term which is not quite significant may be needed in order to produce an adequate fit. Although inconsistencies may occur, with experience in assessing models, acknowledgement that the significance tests are only approximate and the judicious application of Occam's razor, a satisfactory model will be found for the majority of data sets.

When population-side or sex-side interaction terms are found to be significant, they are often associated with one side only. A significant value for only 'x.l', say, should not be interpreted as meaning that only the left side shows a sex difference. Only the more strongly affected of the two sides may appear to be significant if both sides contain essentially the same information.

2. *The parameter estimates.*

When a certain model has been chosen as adequately representing the data, the parameter estimates and their standard errors may be examined. A significant parameter value implies that that particular term is significant, but the t-distribution is again only approximate, so that the deviance associated with a term is a better indicator of its significance (Baker and Nelder 1978).

Despite this warning, examination of the parameters may prove useful. If the difference between the parameters for 'l' and 'r' is significant, this indicates that the trait incidence differs on the two sides. Also, although the deviance may indicate that 'x.l' and 'p.r', say, are significant, only examination of the parameters will reveal which sex the

trait is more common in, or which of the six groups show the greatest difference in trait incidence from the others.

The GLIM program takes one level of each of the factors (i.e. one cell of the table) as a reference level, with parameter values of 0, so that the parameter values for all other levels describe cell values relative to the reference cell. In this analysis of traits, the standard levels are Giza, males and absence of the trait (on both sides). As an example, a negative parameter value for 'r(2)', i.e level 2 (presence) of factor r, indicates that the number of right sides showing the trait is less than the number without it. Likewise, if 'x(2).l(2)' (trait presence on the left in sex level 2, i.e. females), say, has a positive parameter value, this implies that the trait is commoner in females.

A second reason for examining the parameters is that occasionally very large standard errors will be encountered. These are associated with tables containing expected cell values of 0. The occurrence of large standard errors may invalidate the whole test, and if the offending term cannot be excluded from the model, the original data may need to be amended by excluding certain factor levels e.g. removing one of the populations from the analysis. Examination of the original data will often bring to light the source of the problem.

4.3.1.2.2. Correlation among the traits.

Testing for correlation among 60 traits involves the study of contingency tables for 1770 trait pairs. Such tables would also need to be constructed for each group and sex studied, so that testing for correlation among traits is not a simple task. For this reason, trait intercorrelations are not tested exhaustively, but attention is focussed on selected groups of traits. The selection of these groups is based on a consideration of such factors as aetiology, anatomical proximity, and the findings of other workers.

Seven groups of traits are studied. These are:

1. Sutural ossicles and anomalies. Ossenberg (1970) found that sutural ossicles were intercorrelated; metopism and fronto-temporal articulation are also studied in this category.

2. Hypostotic traits.

3. Sutural variations (hypostotic).

4. Hyperostotic traits.

5. Emissary foramina.

6. Traits of the frontal and supraorbital region.

7. Zygomatic foramina.

For the larger groups, the tests employed are Chi-square tests, with or without Yates's correction, and also Pearson's exact probability statistic for two-by-two tables. The BMDP program P4F (Frequency Tables) is used to carry out these tests. Three populations (with the sexes pooled) are tested, Giza, Naqada and Kerma. Although pooling of the sexes could be criticised, it is an expedient necessitated by the rarity of many of the traits. For bilateral traits, the left side of the skull is used. Where correlations found in one group are not reflected in the others, GLIM is used to examine the trait in all six groups, to see if an overall correlation is apparent. For some of the smaller trait categories, GLIM alone is used.

4.3.1.2.3. Inter- and intra-worker error in trait scoring.

Finally, the degree of interworker error is investigated. A subsample of 40 crania from Naqada was scored on two occasions, three months apart, several other groups having been examined in between. For both ordinal and binary scores, the percentage of scores which differ on the two occasions are recorded. Additionally, the trait incidence values are derived, to determine if there has been drift in the scoring, rather than random fluctuation.

The difficulty of defining traits is also investigated by comparison of the trait incidences derived by two different workers. Two samples of thirty crania which had been scored by A.C. Berry (Berry, Berry and Ucko 1967) were again scored by the author, the code numbers having been obtained from A.C. Berry.

The results of the preliminary analysis enable the original battery of 60 traits to be reduced to a smaller number, having excluded those traits which are sex-linked,

intercorrelated or subject to an unacceptably high level of intra-worker error. Measures of divergence can now be calculated from this subsample of 'reliable' traits.

4.3.2. Construction of the distance matrices.

4.3.2.1. Metric traits - the Mahalanobis distance.

The matrices of Mahalanobis' distances are derived using a GENSTAT program (written by Dr. S. P. Evans and the author) to calculate D^2 from the formula given in section 3.2.2. This program (which is listed in appendix 4) derives the dispersion matrix S from complete crania only; however, all available values are used to derive the group means. Matrices of D^2 values are derived for the 6 African groups for each sex separately, and for different numbers of traits. The seven much smaller Greek and Cretan samples are then included. Distances for pooled sexes, and for males only are derived, so that the consequences of pooling the sexes to increase sample size can be examined

Up to 9 of the 10 recorded variables are used in the multivariate analyses. Orbital breadth (OBB) is excluded, since the measurement is defined differently by different workers. Where possible a canonical variate analysis is also undertaken using the modified GENSTAT 'CVAID' subroutine, which produces Mahalanobis distances and also calculates their significance (F-values).

4.3.2.2. Non-metric traits - the Grewal-Smith MMD.

Trait incidences are calculated for all 60 traits using the method of Zegura (1975) for dealing with bilateral traits. Two tables of incidences are derived; left side plus midline and right side plus midline. The Freeman-Tukey formula is used to transform the trait incidences and calculate the MMDs. Variances are calculated according to the method of Sjøvold (1973). Distance matrices are generated for the 6 African groups, using either the left or right side incidences, for pooled and separate sexes, and with varying numbers of traits.

4.3.3. Generation of co-ordinate points and the production of plots.

Once the distance matrices have been generated, an ordinal scaling method is used to transform them into tables of coordinate points. This is done using MINISSA, a program

from the MDS(X) series (Multidimensional Scaling Programs - University of Edinburgh, Program Library Unit). Coxon (1982, pp.43 - 92) gives a detailed account of this technique, but briefly, the theory is as follows. The data in the distance matrix are interpreted, not as actual distances, but as approximate or distorted estimates of the distances, and only their rank order is thought to contain significant information. The aim of the analysis is to turn such data into a set of genuine Euclidian distances. The solution, a set of points in a small number of dimensions, is derived such that the inter-point distances reflect the rank order of the data values as closely as possible. The program creates an initial configuration whose distances are tested against the original data. The badness of fit (stress) is determined, and if unacceptably high, the configuration is improved and retested. This procedure continues until the final configuration is reached, where the stress value either reaches zero, or shows a negligible improvement over the previous value. The *coefficient of alienation*, K (having values between 0 and 1 where 0 indicates a perfect fit) provides a convenient index of the final degree of fit.

Coordinates are generated for each matrix in a number of dimensions. As the number of dimensions rises, K falls, and a configuration of p points will always fit perfectly into p-2 dimensions. Consequently, for 6-group analyses, solution in 4, 3 and 2 dimensions are tested, whereas for 13-group plots up to 9 dimensions are investigated. Subsequently, an adequate solution in the lowest number of dimensions is chosen, with the constraint that the dimensionality be the same for all the plots which will later be compared. MINISSA can process either Mahalanobis' distances (D) or D^2 values (since only their rank order is important), but it does require positive values, so an arbitrary figure (1.00) is added to each MMD value to compensate for the presence of negative numbers.

The three-dimensional coordinates are plotted, using a graphics program written in GINO by Mr.D. Rogers of the Bristol University Computer Centre.

4.3.4. Comparison of the plots - Procrustes rotation.

The last step in the analysis involves the comparison of plots. A GENSTAT program is used to perform Procrustes analysis and give some indication of the degree of agreement

between two plots. For an account of the theory behind this technique consult Gower (1971) or Mardia, Kent and Bibby (1979). Briefly, two sets of points are connected at their centroids and one set is reflected, rotated and scaled until the total distance between corresponding points is minimised. The sum of squared distances (R^2) between corresponding points may be used as a relative measure of general fit; the method used here also scales the plots so that they both have a unit sum of squared distances from the centroid. Under these circumstances R^2, the residual sum of squares, lies between 0 and 1, where 0 indicates perfect congruence between the two plots. This method is used to construct a table of R^2 values from which conclusions regarding the sex independence and taxonomic congruence of the traits can be drawn.

5

RESULTS

The results are presented as follows:

1. Preliminary analysis of the data, for metric and non-metric traits
2. A comparison of morphological distances for 6 African groups.
3. A comparison of morphological distances for 13 Greek and African groups.

More attention is given to the 6 African groups because of their larger sample sizes. Though the Greek samples are arguably too small for the inclusion in either metric (Van Vark 1976, McHenry and Corruccini 1975) or non-metric (Berry 1975, Sjøvold 1973) studies, analysis of all 13 groups is undertaken for three reasons;

1. to attempt to confirm the results of the 6 group analyses.
2. to test whether pooling of the sexes in metric studies is legitimate.
3. to assess the population affinities of the groups as revealed by both methods, which is, after all, the motive for undertaking this type of study.

The appendices contain summaries of the raw data, and the results of some basic statistical tests (metric in appendix 1, non-metric in appendix 2). Examples of output from the GLIM package which illustrate its use for investigating sex and side effects in non-metric data, are also presented in Appendix 3.

5.1. Preliminary analysis of the data.

5.1.1. Metric data.

5.1.1.1. Basic statistics.

For each of the 13 groups, 10 measurements were examined in males and females. The mean, range, variance, standard deviation and coefficients of skewness and kurtosis were generated using the GENSTAT subroutine 'BASIC'. These statistics are reproduced in tables

A1.1.1 to A1.1.10 in appendix 1. The coefficient of skewness reached significance only once in 239 tests; however, significant levels of positive and negative kurtosis (indicating respectively that the curve is flatter or taller than expected) were frequently encountered. Out of 234 tests where a value could be calculated, 55 (23.5%) gave a significant positive value and 7 (3%) a significant negative value.

These results challenge the assumption that skull measurements are normally distributed variables; whether this finding has any practical effect on the multivariate techniques used is a different question. It could be argued that skewness represents a more serious departure from normality than kurtosis, and there is no evidence of skewness in the data. Furthermore, the robustness of multivariate methods to departures from normality have been repeatedly emphasised (e.g. Blackith and Reyment 1971, Chatfield and Collins 1980). It does however raise doubts about the validity of homogeneity tests, and not too much emphasis will therefore be placed on the results of these tests.

5.1.1.2. One-way analysis of variance.

This test was carried out using the MINITAB statistical package. For each group the males were tested; among the females, some groups had fewer than 4 measurements, and these groups were excluded from the test. This test also produces plots of the 95% confidence intervals for the group means. The computer output from these tests is shown in appendix 1 (tables A1.2.1 to A1.2.10). The F-values (ratio of between-group to within-group variance) obtained from the one-way analysis of variance are reproduced in table 5.1. Out of 26 tests, all but one (orbital height in females) gave a significant ($p < 0.05$) value, indicating that the means of each of the 10 measurements differ significantly among the groups. It is also noticeable that the breadth measurements (especially orbital, nasal and maximum cranial breadth) appear to be the strongest discriminators between the groups. In general, this test confirms that the 10 measurements chosen (with the possible exclusion of orbital height) are suitable candidates for inclusion in a multivariate analysis.

TABLE 5.1

ONE-WAY ANALYSIS OF VARIANCE OF 10 MEASUREMENTS

IN CRANIA FROM 13 SITES.

	MALES ONLY		FEMALES ONLY	
	F-value	groups	F-value	groups
GOL	3.94**	all sites	3.80**	minus AG
BNL	2.73**	all sites	2.16*	minus AG, MP
XCB	20.81**	all sites	18.11**	minus MP
ZYB	7.21**	all sites	8.38**	minus AG, FT, MP
NPH	5.75**	all sites	8.97**	minus AG, FT, MP
NLH	4.44**	all sites	5.85**	minus AG, FT, MP
OBH	2.80**	all sites	2.04	minus AG, FT, MP
OBB	16.23**	all sites	22.04**	minus AG, FT, MP
NLB	10.28**	all sites	19.65**	minus AG, FT, MP
ZMB	4.50**	minus FT	5.63**	minus AG, FT, MP

* - $p < 0.05$

** - $p < 0.01$

The F-value is the ratio of the between-group to the within-group variance.

The sites above are identified by the following codes:

AG - Athens-GA FT - Fortetsa MP - Myrtos Pyrgos.

5.1.1.3. Tests of homogeneity of the dispersion matrices.

For this test a modified version of the GENSTAT macro 'CVAID' is used. The following data sets are analysed:

1 6 African groups, males only
9 variables (GOL, BNL, XCB, ZYB, NPH, NLH, OBH, NLB, ZMB)

2 6 African groups, females only
9 variables (GOL, BNL, XCB, ZYB, NPH, NLH, OBH, NLB, ZMB)

3. 11 African and Greek groups, males only
5 variables (GOL, XCB, NPH, OBH, NLB)

4. 11 African and Greek groups, males and females combined.
5 variables (GOL, XCB, NPH, OBH, NLB)

5. 5 Greek groups, males only
5 variables (GOL, XCB, NPH, OBH, NLB)

6. 5 Greek groups, males and females combined.
5 variables (GOL, XCB, NPH, OBH, NLB)

The 6 African groups are examined, for both sexes, using 9 measurements. It is not possible to test these 9 measurements for all 13 groups, as CVAID requires complete data, and the Greek samples are too small and fragmented. Only 5 variables are studied; even so, the poorly preserved Cretan groups have to be excluded. There are too few intact females in the Greek samples to allow a separate analysis of that sex, so males and pooled sexes are tested. Finally the males and pooled sexes from the 5 Greek sites are examined.

The statistic of choice is the F-statistic suggested by Box (1949, see also Morrison 1967, p 153). The F-values are shown in table 5.2. Most of the values are not significant, indicating that the group dispersion matrices are homogeneous. The only value to reach significance is, not surprisingly, that for the pooled sexes in the 11 group analysis, where the sex ratio in each group varies widely. The pooled-sex group in the 5 group analysis falls just short of the 5% level of significance. This result could be interpreted as invalidating those metric studies where, for reason of sample size, the sexes are combined. Before condemning such studies, however, it could be remarked that the F-value is not greatly significant, and that multivariate methods are known to be robust, whereas homogeneity tests are sensitive to departures from normality.

TABLE 5.2

HOMOGENEITY OF THE DISPERSION MATRICES

(USING BOX'S (1949) F-TEST)

Analysis	F-value	df1	df2
6 African groups 9 variables - males	1.090	225	57738
6 African groups 9 variables - females	1.104	225	13340
11 Greek & African groups 5 variables - males	1.121	150	6483
11 Greek & African groups 5 variables - pooled sexes	1.380*	150	11429
5 Greek groups 5 variables - males	1.189	60	2107
5 Greek groups 5 variables - pooled sexes	1.381	60	3432

* - $p < 0.05$

5.1.1.4. The significance of metric distances

The CVAID macro, as well as testing the dispersion matrices, also calculates significance values for the Mahalanobis distances. The methods used in section 5.2 calculate D^2 using data from whole and broken skulls, but do not (unlike the non-metric methods) generate significance statistics. These D^2 values differ from those derived by CVAID (which, in general, are derived from a smaller intact subset of crania), but their significance values are nonetheless worthy of inspection.

Two statistics are produced. The first tests for the overall equality of the group means, producing an F-value which is a transformation of Wilks' Lambda (Blackith and Reyment 1971). The second is a 'distance matrix' of F-values, again a transformation of the Hotelling T^2 test (Chatfield and Collins 1980) indicating the significance of individual D^2s. The D^2s, their F-values and the overall F-value are shown in appendix 1 in tables A1.3 to A1.8. Discussion of these values is deferred to section 5.3.4

5.1.2. Non-metric data.

5.1.2.1. Sex and side interactions.

53 bilateral traits are examined using GLIM to determine the following:

1. Whether the left and right sides are independent.
2. Whether the trait incidence is the same on the left and right sides.
3. Whether the trait incidence is dependent on the sex.
4. Whether the trait incidence is dependent on the population.
5. Whether more complex sex, side and population interactions are present in the data.

It is not possible to answer all of these questions for every trait since the rarer traits produce contingency tables with too many zero cells for a satisfactory full analysis. The results, however, aid in deciding which of the various methods proposed for the recording of bilateral traits is the most appropriate, and which individual traits do not match the assumptions inherent in the measure of divergence.

RESULTS

The remaining 7 midline traits are also tested for sex dependence. Trait 23, 'palatine torus present', was found amongst the Egyptian and African groups only as trace, as was the bilateral trait 24, 'maxillary torus present', and these are tested as such, so that they can be included in the analysis, though traces are regarded as absent in the calculation of the measure of divergence.

1. *Independence of right and left sides.*

Only 2 traits (3.8%) are found in which the left and right sides do not appear to be significantly correlated. These are:

7. Coronal ossicle, and
20. Foramen ovale and spinosum continuous.

This is overwhelming evidence that the two sides of the skull are not independent of each other with regard to the expression of non-metric traits. The use of both sides as separate units in determining trait incidence as advocated by Berry and Berry (1967), and Kellock and Parsons (1970a) among others, cannot therefore be recommended.

2. *Equality of trait incidence on the right and left sides.*

Green, Suchey and Gokhale (1979) state that their method of determining trait incidence rests on the assumptions that the right and left sides are correlated and that the 'true' trait incidence is the same on both sides. Listed below are those 8 traits (15.1% of the bilateral traits studied) for which a significant difference in right and left incidence is found:

4. Parietal foramen	(more common on the right).
15. Mastoid foramen absent	(more common on the left).
18. Precondylar tubercle	(more common on the left).
30. Accessory infraorbital foramen	(more common on the left).
32. Infraorbital suture	(more common on the right).
36. Trochlear spur	(more common on the right).
45. Intermediate condylar canal	(more common on the right).
58. Pterygoid spurs	(more common on the left).

This result reinforces the contention that Zegura's (1975) method is the one of choice. Though information is lost where one side only is considered, no assumptions are inherent in the method, and distances derived from the left side can be compared to those calculated using the right. Hence the traits listed above need not be excluded from the MMD for this reason, though workers using the formula of Green, Suchey and

Gokhale would be well advised to check their data for unequal left and right side incidence before proceeding further.

3. *Dependence of trait incidence on sex.*

Seven traits are found to have a higher incidence in one sex, representing 11.7% of the 60 traits studied. Since pooling of the sexes is said to be one of the many advantages which non-metric traits have over metric ones, these traits are excluded from calculations where the sexes are pooled. The sex linked traits are:

8. Epipteric bone	(more common in females).
13. Foramen of Hüschke	(more common on the left in females).
15. Mastoid foramen absent	(more common on the right in females).
19. Hypoglossal canal bridge	(more common on the right in males).
30. Accessory infraorbital foramen	(more common on the right in females and on the left in males).
32. Infraorbital suture	(more common on the left in females).
48. Pharyngeal tubercle	(midline - more common in males).

There is also a suggestion that two further traits, 'pterygo-basal bridge' (no.52) and 'Inca bone present' (no.31) may be sex related, though the rarity of these traits makes the interpretation of such a link difficult, since in both cases the minimum model provides a sufficiently good fit to explain the data.

4. *Dependence of trait incidence on population.*

In several traits the incidence is found to be related to the population. This test does not give grounds for exclusion of a trait but rather emphasises those traits which discriminate between the groups studied, and which would be expected to form the largest contribution to the ultimate measures of divergence between the groups. These traits are:

3. Lambdoid ossicle	(p.r significant).
4. Parietal foramen	(p.r significant).
14. Mastoid foramen exsutural	(p.r significant).
32. Infraorbital suture	(p.l and p.r significant).
33. Nasal sill sharp	(p.r significant).
34. Nasal foramen	(p.l significant)
37. Trochlear fossa	(p.l and p.r significant).
43. Zygomatico-orbital foramen	(p.r significant).
44. Occipito-mastoid ossicle	(p.r significant).
45. Intermediate condylar canal	(p.r significant).
48. Pharyngeal tubercle	(midline).
55. Foramen ovale spine	(p.r significant).
56. Accessory foramen spinosum	(p.l significant).

Amongst the bilateral traits, the right side appears more frequently to discriminate between the groups, which suggests that for these data, divergences derived from the right side may be more useful than those derived from the left.

5. *Dependence of trait incidence on complex factor-interactions.*

For a few traits, the model produced after the inclusion of all individual factors and two-factor interactions is not sufficient to produce a good fit with the data. In these cases, three-factor interactions are introduced and tested for significance. Such factors indicate that sex and side interactions, or left-right interactions vary respectively from group to group or with sex or group. This may reflect different genetic or environmental influences on trait expression among the groups and sexes, or it may reflect errors in the subjective scoring of the traits which mask any underlying biological pattern.. Whatever the reason, the traits listed below are best excluded from further analysis.

8. Epipteric bone, and
13. Foramen of Hüschke present.

The remaining traits may be divided into those in which no significant side-sex or side-population interactions are apparent and those where the 'minimum model' alone provides a sufficiently good fit to the data. In the latter only left-right interactions are tested, but even where a significant value for left-right interaction is obtained, the existence of such an interaction is not certain. 'Minimum model' traits are generally rare traits where there is insufficient data for a full analysis, and though they are not excluded from the calculation of divergence this does not mean that their suitability is proved; much larger samples are required to do this. Traits for which the minimum model alone provides a sufficiently good fit are:

7. Coronal ossicle
17. Bifaceted condyles
20. Foramen ovale and spinosum continuous
39. Squamo-parietal ossicles
46. Postcondylar tubercle
50. Foramen ovale incomplete
52. Pterygo-basal bridge
53. Pterygo-spinous bridge
56. Accessory foramen spinosum
57. Lateral pterygoid perforated

Traits which show no significant sex or population effects are:

1. Highest nuchal line
10. Parietal notch bone
11. Ossicle at asterion
12. Auditory torus
16. Postcondylar canal patent
21. Foramen spinosum open
24. Maxillary torus
25. Zygomatico-facial foramen absent
26. Supraorbital foramen complete
27. Frontal notch or foramen
28. Anterior ethmoid foramen exsutural
29. Posterior ethmoid foramen absent
33. Nasal sill sharp
36. Trochlear spur
38. Frontal grooves
40. Os Japonicum trace
41. Processus marginalis
42. Zygomatico-temporal foramen
47. Jugular foramen bridge
51. Foramen of Vesalius
54. Spino-basal bridge
59. Palatine bridge
60. Zygomatico-facial foramen multiple

For three remaining traits the interpretation of the GLM was not straightforward. The results for these traits will be described individually. They are:

9. Fronto-temporal articulation
18. Precondylar tubercle
22. Accessory lesser palatine foramina

9. Fronto-temporal articulation.

The minimum model did not provide a sufficiently good fit. The five two-factor terms were then added to the model. The residual scaled deviance was not significant (15.99 for 21df), denoting a good fit, so three-factor terms were not tested. When each of the two-factor terms were in turn excluded, l.r and p.l were found to be significant (64.86 for 1df; $p < .001$ and 12.39 for 5df; $p < .05$ respectively). However, examination of the parameters for the minimum model plus the terms p.l and l.r revealed large standard errors in relation to presence of the trait on the left in group 4. Perusal of the contingency table showed that in group 4 only, the trait was never present on the left, and thus the high standard errors arose where the model attempted to define a logarithmic coefficient to give an expected cell value of zero (the log of zero being minus infinity).

It may be noted that the level of significance of p.l is not very high and, remembering that the asymptotic log-likelihood distribution only approximates the Chi-square distribution, this result may not after all denote a significant effect. When p.l was removed from the model it was found that the minimum model plus l.r provided an adequate fit.

Confirmation of this was found when the test was repeated with group 4 excluded; p.l no longer had a significant effect.

The interpretation of the model for this trait is that there is no evidence of three-factor interactions or of sex or population effects in the data. The left and right sides are not independent and examination of the parameters for the left and right side factors (l and r) show that trait incidence on both sides is not significantly different (difference = +0.693, S.E = 0.611). There is no evidence to advocate discarding this trait.

18. Precondylar tubercle.

The minimum model did not provide a sufficiently good fit. The remaining two-factor terms were then added to the model, resulting in a sufficiently good fit to preclude the possibility of more complex interactions. Of the five two-factor terms, only l.r was found to be significant (117.32 for 1df), but the scaled deviance of the minimum model plus l.r was too large (53.83 for 33df) to adequately explain the data. The largest remaining two-factor term (p.l at 7.84 for 5df) was then included, resulting in an adequate fit (scaled deviance of 39.64 for 28df). The largest sex-related factor, x.l, was also added, with l.r, to the minimum model, but this did not produce an adequate fit (50.12 for 32df).

In conclusion, there is no evidence of three-factor interactions or sex effects in the data, but it is possible that this trait does discriminate between populations and may usefully be included in the traits from which the mean measure of divergence is derived. The left and right sides are not independent and examination of the coefficients reveals that this trait is more commonly present on the left (difference = +1.211, S.E.=0.393; for 28df, this value is significant at $p < .001$).

22. Accessory lesser palatine foramina.

After fitting all the single and two factor terms, the residual scaled deviance was found to be just significant (35.25 for 21df; $p < .05$). The four three- factor interactions were then added to the model and then excluded in turn to test their significance. The term p.x.l was highly significant (23.21 for 5df; $p < .001$). Any two factor terms included in the expression

p.x.l (i.e. p.x, x.l, p.l) must be included in the model, but the remaining terms were tested by exclusion. The term l.r, being significant, was included while the others were discarded.

In this model, however, all the terms relating to group 6 (p, p.x, p.l, p.x.l) had parameters with large standard errors. The trait contingency table showed that in group 6 males the trait was never absent on the left so that expected cell values of zero account for these high standard errors. However, the model based on one and two-factor terms alone may probably be regarded as sufficient as the chi-square value is not very significant, especially as when the test was repeated excluding group 6, one and two factor terms alone produced an adequate fit (residual deviance of 24.61 for 17df).

The test was then repeated for all six groups without fitting three-factor terms. The terms l.r and x.l were significant (30.58 and 6.05 for 1df; $p < .001$ and .025 respectively), but the model including only significant terms did not adequately describe the data (residual deviance = 55.38 for 32df; $p < .01$). The term p.r, which approached significance (10.55 for 5df), was therefore added but even then the residual deviance was too high (43.45 for 27df; $p < .025$).

This trait proved one of the most difficult to interpret, but it should probably not be used as there is some evidence of a sex effect on its incidence on the left, which may vary in different populations. The left and right sides are not independent and incidence on both sides is not significantly different from zero (difference = -0.445, S.E = 0.414).

5.1.2.2. Correlations between the traits.

For all tests of correlation, the sexes were combined to increase the sample size. For bilateral traits, only the left side of the skull was considered. Chi-square tests (with Yates's correction where necessary) and Pearson's exact probability test were used for the three largest groups (Giza, Kerma and Naqada). Where the Chi-squares indicated more correlations than could be explained by chance, GLIM was used to model the distribution of those two traits in all six groups.

Sutural ossicles and anomalies.

The following traits were examined in pairs for correlation:

2. Ossicle at lambda	9. Fronto-temporal articulation
3. Lambdoid ossicle	10. Parietal notch bone
5. Bregmatic bone	11. Ossicle at asterion
6. Metopism	31. Inca bone
7. Coronal ossicle	39. Squamo-parietal ossicle
8. Epipteric bone	44. Occipito-mastoid ossicle.

Out of 187 Chi-square tests, 15 gave significant values, where 9 or 10 would be expected by chance, and all the correlations were positive.

The 66 trait pairs were then tested with GLIM. The following pairs were found by both methods to be correlated:

2. Ossicle at lambda	with	3. Lambdoid ossicle
3. Lambdoid ossicle	with	7. Coronal ossicle
3. Lambdoid ossicle	with	10. Parietal notch bone
8. Epipteric bone	with	39. Squamo-parietal ossicle
10. Parietal notch bone	with	11. Ossicle at asterion
11. Ossicle at asterion	with	39. Squamo-parietal ossicle

Traits 3 (lambdoid ossicle) and 11 (ossicle at asterion) were correlated in one group (Kerma); GLIM also revealed an interaction but a simpler model without correlation could also adequately describe the data. Traits 5 (bregmatic bone) and 6 (metopism) were strongly correlated in one group (Giza), but this association was not quite significant for all six groups. The GLIM analysis also revealed an association between traits 3 (lambdoid ossicle) and 6 (metopism), which was not shown by the Chi-square test. Ossenberg's (1970) conclusion that sutural ossicles are in general correlated is therefore supported by this data.

Hypostotic traits.

Three 'hyperostotic' traits were studied using GLIM:

21. Foramen spinosum open	49. Pharyngeal fossa
37. Trochlear fossa	

No significant associations were found.

Sutural variations.

Three sutural traits were examined:

6. Metopism	40. Os Japonicum trace
32. Infraorbital suture	

Chi-square tests showed no significant interaction between them.

Hyperostotic traits.

Fourteen 'hyperostotic' traits were tested:

1. Highest nuchal line
18. Precondylar tubercle
33. Nasal sill sharp
36. Trochlear spur
41. Processus marginalis
45. Intermediate.condylar canal
47. Jugular foramen bridge
48. Pharyngeal tubercle
52. Pterygo-basal bridge
53. Pterygo-spinous bridge
54. Spino-basal bridge
55. Foramen ovale spine
58. Pterygoid spurs
59. Palatine bridge

Out of 260 Chi-square tests, 4 tests were significant, and two of these correlations were negative. This is far fewer than the 13 expected by chance, and analysis with GLIM was not undertaken. It is therefore concluded that hyperostotic traits are, in general, uncorrelated.

Emissary foramina.

The following traits were studied:

4. Parietal foramen
15. Mastoid foramen absent
16. Postcondylar canal patent
51. Foramen of Vesalius

Of the 18 Chi-square tests, 1 significant value was found, but GLIM analysis revealed no significant interaction, and it was concluded that these traits are uncorrelated.

Frontal and supraorbital traits.

The following traits were studied:

26. Supraorbital foramen complete
27. Frontal notch or foramen
38. Frontal grooves

These traits share a common aetiology, representing differential growth of the nervous and bony elements in the frontal region. Of the 9 Chi-square tests undertaken, 4 showed significant associations; in all three groups frontal grooves were correlated with presence of the frontal foramen. In skulls from Giza, supraorbital and frontal foramina were also strongly correlated. Analysis of these three traits with GLIM confirmed these two associations. The following pairs are therefore positively correlated;

26. Supraorbital foramen complete	with	27. Frontal notch or foramen
27. Frontal notch or foramen	with	38. Frontal grooves

Dixon's (1904) observation that the presence of frontal grooves correlates with the depth of the supraorbital notch could not be confirmed.

Zygomatic foramina.

Four foraminal traits are found in the zygomatic region:

25. Zygomatico-facial foramen absent
42. Zygomatico-temporal foramen
43. Zygomatico-orbital foramen
60. Zygomatico-facial foramen multiple

It has been noted during the individual trait descriptions (section 4.2.2) that the trait 'zygomatico-facial foramen multiple' can reasonably be scored only when at least one foramen is present. Total absence of a foramen implies that the trait can not be recorded (cf. mastoid f. absent and exsutural). Consequently, traits 25 and 60 are not tested for correlation with each other.

The 15 Chi-square tests show 4 significant associations. In all three groups, traits 25 and 43 are strongly negatively correlated i.e. if one foramen is absent, the other is more likely to be absent too. This is not surprising, since the foramina join to form the zygomatico-facial canal. In the crania from Giza alone, trait 25 and 42 are strongly (positively) correlated, implying that presence of the zygomatico-temporal nerve is more common when the zygomatico-facial nerve is missing.

The GLIM analysis confirmed this pattern; traits 25 and 43 interact strongly while 25 and 42 have a weaker but significant association. Traits 42 and 43 are not significantly correlated with each other, or with trait 60. Hence the following trait pairs are correlated;

25. Zygomatico-facial foramen absent with 42. Zygomatico-temporal foramen
25. Zygomatico-facial foramen absent with 43. Zygomatico-orbital foramen

Exclusion of inter-correlated traits.

If the following six traits are excluded from the MMD, then significant trait intercorrelations will be avoided while maximising the number of traits which can be used.

3. Ossicle at lambda
8. Epipteric bone
11. Ossicle at asterion
27. Frontal foramen or notch
42. Zygomatico-temporal foramen
43. Zygomatico-orbital foramen

5.1.2.3. Error in scoring the traits.

a. Intra-worker error.

Intra-worker error was investigated using a subset of 46 skulls from Naqada. These skulls were measured on two occasions, several months apart, and the concordance between the scores was noted. The results are presented in tables 5.3 and 5.4. Cases where the trait was thought unscorable or missing on one or both occasions are excluded from this analysis. For each trait the percentage of mismatching scores is given. Scoring errors may be random or directional, the latter type representing 'drift' in the setting of the threshold for trait definition. Since several other series of crania were examined in between, such drift is likely to have occurred. Drift is assessed by considering the difference in the sample incidence of the traits derived on each occasion.

The degree of error is related to the rarity of the trait, rare traits necessarily having a lower percentage mismatch, and incidences derived from the first occasion are shown as an aid to the interpretation of the errors. Incidences for bilateral traits are calculated using both sides of the skull to maximise the information in the data. This is justifiable since these incidences are not used to derive a measure of divergence.

Table 5.3 contains those traits which are allocated a binary score in the field. The percentage mismatch, initial incidence and difference in incidence values are shown. Table 5.4 contains those traits which are allocated an ordinal score in the field and later dichotomised for further analysis. The scoring categories and threshold levels are shown, along with the percentage mismatch for both the ordinal and the dichotomised scores.

Although this method of quantifying error is crude, the results are disquieting. While most (35, or 58%) of the 60 traits have scoring errors below 5%, 15 (25%) show discrepancies of over 10%, and 4 (3.3%) of over 20%. Ordinal scoring is particularly susceptible to error; out of 29 traits only 2 (7%) had ordinal discrepancies lower than 5%, and 24 (83%) exceeded the 10% level. This result throws further doubt on the utility of ordinal scoring methods.

TABLE 5.3

INTRA-WORKER ERROR IN THE RECORDING OF NON-METRIC TRAITS.

TRAITS WITH BINARY SCORES.

	% mismatch in raw score	Trait frequency on the first occasion.	Difference in trait frequency.
1. HiNuLin	29.3	59.8	7.6
2. OsAtLam	2.2	10.9	-2.2
5. OsBreg	0.0	2.2	0.0
7. OsCoron	0.0	2.2	0.0
8. OsPter	4.4	14.3	-2.2
9. FrTemAr	3.3	2.2	-1.1
10. OsPaNot	7.6	12.0	1.0
11. OsAster	1.1	4.4	-1.1
12. TorAud	2.2	2.2	2.2
13. FHusch	1.1	16.5	-1.1
14. FMasEx	6.0	41.0	4.6
15. FMasAb	19.6	33.7	4.3
20. FOvSpOp	0.0	3.3	0.0
21. FSpOp	8.8	17.6	-6.6
28. FAEthEx	21.4	47.2	-7.9
29. FPEthAb	3.5	2.4	1.1
30. FIOrbAc	5.4	7.6	1.1
31. OsInca	0.0	0.0	0.0
33. NasSill	14.1	78.3	14.1
34. FNasal	15.7	77.1	15.0
38. GrFront	15.4	19.6	13.4
39. OsSqPar	1.1	2.2	-1.1
40. SuJapTr	4.8	2.2	2.6
42. FZyTem	17.4	57.6	10.7
43. FZyOrb	4.4	92.2	3.1
44. OsOcMas	4.3	6.5	-2.0
50. FOvOp	1.1	1.1	1.1
55. SpinFOv	4.4	3.3	-2.2
56. FSpAc	2.2	2.2	0.0
57. PerfPt	4.0	5.0	1.6
60. FZyFMu	3.3	37.0	0.3

TABLE 5.4

INTRA-WORKER ERROR IN THE SCORING OF NON-METRIC TRAITS.

TRAITS WITH ORDINAL SCORES.

Trait	Ordinal scores	Mismatch in raw ordinal scores (%)	Mismatch in raw binary scores (%)	Trait frequency on 1st occasion (%)	Difference in trait frequency (2nd-1st)
3. OsLambd	0 / 1 2..	14.1	6.5	32.6	0.0
4. FPariet	0 1 / 2	14.4	7.8	41.3	7.6
6. SuMetop	0 1 / 2	26.1	0.0	2.2	0.0
16. CanConP	0 1 / 2	11.0	5.5	61.5	2.6
17. BifaCon	0-2 / 3 4	12.5	0.0	0.0	0.0
18. TubConA	0 / 1-3	13.4	6.6	15.4	4.2
19. BrCanHy	0-3 / 4	18.5	4.3	19.6	2.1
22. FLPalAc	1 \ 2 3..	42.0	8.0	86.4	4.8
23. TorPal	0 1 / 2	8.9	0.0	0.0	0.0
24. TorMax	0 1 / 2	7.6	0.0	0.0	0.0
25. FZyFAb	0 \ 1 2..	13.2	4.4	20.7	-3.1
26. FSupOrb	0-3 / 4	12.0	4.3	18.5	0.0
27. FNotFr	0 1 / 2	2.2	2.2	8.7	0.0
32. SuIOrb	0 1 / 2	27.5	13.2	33.7	13.2
35. CribOrb	0 1 / 2 3	13.0	2.2	9.8	-2.2
36. SpurTro	0 / 1-3	3.3	1.1	17.4	-0.9
37. FosTro	0 1 / 2 3	31.9	15.4	35.9	7.0
41. ProcMar	0 1 / 2	20.9	2.2	3.3	2.2
45. CanConI	0-2 / 3 4	44.0	30.8	35.2	28.9
46. TubConP	0 1 / 2 3	7.8	0.0	0.0	0.0
47. BrJugF	0-2 / 3 4	39.1	12.0	10.9	11.9
48. TubPhar	0 1 / 2 3	17.4	8.7	26.1	4.3
49. FosPhar	0 1 / 2 3	23.9	15.2	26.1	-6.5
51. FVesal	0 1 / 2	23.1	11.0	26.4	-2.5
52. BrPtBas	0-2 / 3 4	22.2	1.1	2.2	-1.1
53. BrPtSp	0-2 / 3 4	34.1	1.2	1.1	1.2
54. BrSpBas	0-2 / 3 4	30.0	3.3	4.4	1.2
58. SpurPt	0 / 1 2..	53.2	43.5	32.4	31.8
59. BrPal	0-2 / 3 4	28.3	13.0	34.8	-6.5

Ordinal scores : the threshold for conversion to binary scores is marked by the following symbols:

/ - values to the right scored present
\ - values to the left scored present.

RESULTS

Drift in the trait frequencies is marked. In 15 traits(25%), the frequencies differ by more than 5% or 0.05. Of the 13 cases where the frequency is identical on both occasions, most represent very rare traits, 5 of which are completely absent from this sample.

b. Inter-worker error.

Traits 1 to 30 were scored in two samples from Kerma and Badari. These samples contained the crania which were studied by Berry, Berry and Ucko (1967). In table 5.5 the trait frequencies obtained by A. C. Berry are compared with the frequencies obtained by the author. Only 16 (53%) of the traits showed inter-worker differences which did not exceed 5% (0.05) for both samples.

Although the above analyses of error are statistically crude, they contradict the assertions that "the scoring of variants by different workers appears to be comparable", and that "a single individual should be consistent in his own classification" (Berry and Berry 1967). Molto (1976) also found considerable inter-worker error in trait scores, though the errors reported here are, in general, higher than his. Similarly, he found that much higher error levels were associated with ordinal scoring methods. Molto demonstrated that such errors could have a significant effect on inter-population distances. It is advisable therefore to omit certain traits whose levels of intra-worker error differs by more than an arbitrarily chosen figure (in this case 15%). These traits are listed below.

1. Highest nuchal line
15. Mastoid foramen absent
28. Anterior ethmoid foramen exsutural
34. Nasal foramen
37. Trochlear fossa
38. Frontal grooves
42. Zygomatico-temporal foramen
45. Intermediate condylar canal
49. Pharyngeal fossa
58. Pterygoid spurs

5.1.2.4. Summary.

A summary of the results of the non-metric preliminary analysis is presented in table 5.6.

TABLE 5.5.

INTER-WORKER ERROR IN TWO SAMPLES FROM

KERMA (50 SKULLS) AND BADARI (48 SKULLS).

Scored by a) J.E.Powell in July, 1987.
b) A.C.Berry (Berry, Berry and Ucko 1967)

DIFFERENCES IN TRAIT FREQUENCIES (%).

	KERMA			BADARI		
	JEP	ACB	Diff.	JEP	ACB	Diff.
1. HiNuLin	51.0	30.0	21.0	52.1	20.8	31.3
2. OsAtLam	8.5	6.0	2.5	10.9	10.4	0.5
3. OsLambd	34.8	26.0	8.8	36.6	30.1	6.5
4. FPariet	52.0	65.0	-13.0	40.9	32.2	8.7
5. OsBreg	0.0	0.0	0.0	0.0	0.0	0.0
6. SuMetop	4.0	2.0	2.0	8.3	6.2	2.1
7. OsCoron	2.4	2.0	0.4	1.2	2.1	-0.9
8. OsPter	17.0	13.0	4.0	20.9	19.0	1.9
9. FrTemAr	12.0	14.0	-2.0	2.2	1.2	1.0
10. OsPaNot	10.2	7.0	3.2	12.8	10.4	2.4
11. OsAster	3.0	3.0	0.0	7.4	9.4	-2.0
12. TorAud	0.0	0.0	0.0	4.3	4.3	0.0
13. FHusch	34.3	38.0	-3.7	14.0	7.6	6.4
14. FMasEx	60.0	52.0	8.0	52.9	35.8	17.1
15. FMasAb	50.0	6.0	44.0	38.1	16.2	21.9
16. CanCon	61.6	34.0	27.6	56.8	28.7	28.1
17. BifaCon	0.0	2.0	-2.0	3.4	0.0	3.4
18. TubConA	7.0	7.0	0.0	11.8	4.7	7.1
19. BrCanHy	12.0	11.0	1.0	17.9	18.0	-0.1
20. FOvSpOp	1.0	1.0	0.0	1.1	1.2	-0.1
21. FSpOp	15.2	23.0	-7.8	13.3	21.5	-8.2
22. FLPalAc	78.0	64.0	14.0	78.8	31.5	47.3
23. TorPal	0.0	0.0	0.0	0.0	0.0	0.0
24. TorMax	0.0	0.0	0.0	0.0	0.0	0.0
25. FZyFAb	17.2	7.0	10.2	21.3	19.2	2.1
26. FSupOrb	10.1	11.0	-0.9	20.4	15.0	5.4
27. FNotFr	17.3	69.0	-51.7	6.3	18.1	-11.8
28. FAEthEx	37.8	16.0	21.8	36.9	33.2	3.7
29. FPEthAb	2.1	2.0	0.1	0.0	0.0	0.0
30. FlOrbAc	4.0	3.0	1.0	4.7	2.5	2.2

TABLE 5.6.

NON-METRIC TRAITS - SUMMARY OF THEIR SUITABILITY

FOR INCLUSION IN POPULATION STUDIES.

	Sex Linked	Correlated with	Scoring errors	Comments
1. HiNuLin	No		v.high	Anthroposcopic ?
2. OsAtLam	No	3	v.low	
3. OsLambd	No	2,6?,7,10,11?	low	
4. FPariet	No		low	L, R frequencies differ.
5. OsBreg	No	6?	v.low	
6. SuMetop	No	5?,3?	v.low	
7. OsCoron	No		v.low	L, R independent ?
8. OsPter	Yes	39	v.low	3-factor interactions.
9. FrTemAr	No		v.low	
10. OsPaNot	No	11,3	low	
11. OsAster	No	3?,10,39	v.low	
12. TorAud	No	-	v.low	NOT GENETIC.
13. FHusch	Yes	-	v.low	3-factor interactions.
14. FMasEx	No	-	low	
15. FMasAb	Yes		high	L, R frequencies differ.
16. CanConP	No		low	
17. BifaCon	No	-	v.low	
18. TubConA	No		low	L, R frequencies differ.
19. BrCanHy	Yes	-	v.low	
20. FOvSpOp	No	-	v.low	L, R independent ?
21. FSpOp	No		low	
22. FLPalAc	Yes	-	low	3-factor interactions ?
23. TorPal	No	-	v.low	trace only in Africans.
24. TorMax	No	-	v.low	trace only in Africans.
25. FZyFAb	No	42,43	v.low	
26. FSupOrb	No	27	v.low	
27. FNotFr	No	26,38	v.low	
28. FAEthEx	No	-	v.high	
29. FPEthAb	No	-	v.low	Missing from Pyrgos.
30. FlOrbAc	Yes	-	low	L, R frequencies differ.

TABLE 5.6 CONTINUED.

NON-METRIC TRAITS - SUMMARY OF THEIR SUITABILITY

FOR INCLUSION IN POPULATION STUDIES.

	Sex Linked	Correlated with	Scoring errors	Comments
31. OsInca	No		v.low	weak sex link ?
32. SuIOrb	Yes		medium	L, R frequencies differ.
33. NasSill	No		high	
34. FNasal	No	-	high	
35. CribOrb	No	-	v.low	NOT GENETIC.
36. SpurTro	No		v.low	L, R frequencies differ.
37. FosTro	No		high	
38. GrFront	No	27	high	
39. OsSqPar	No	8,11	v.low	
40. SuJapTr	No		low	
41. ProcMar	No		v.low	
42. FZyTem	No	25	high	
43. FZyOrb	No	25	v.low	
44. OsOcMas	No		v.low	
45. CanConI	No		v.high	L, R frequencies differ.
46. TubConP	No	-	v.low	
47. BrJugF	No		medium	Scoring method varies.
48. TubPhar	Yes		low	
49. FosPhar	No		high	
50. FOvOp	No	-	v.low	
51. FVesal	No		medium	
52. BrPtBas	No		v.low	weak sex link ?
53. BrPtSp	No		v.low	
54. BrSpBas	No		v.low	
55. SpinFOv	No		v.low	
56. FSpAc	No	-	v.low	
57. PerfPt	No	-	v.low	
58. SpurPt	No		v.high	L, R frequencies differ.
59. BrPal	No		medium	
60. FZyFMu	No		v.low	

Scoring errors - v.low - fewer than 5% of binary scores differ.
low - between 5% and 10% of binary scores differ.
medium- between 10% and 15% of binary scores differ.
high - between 15% and 20% of binary scores differ.
v.high- more than 20% of binary scores differ.

In the 'correlated with' column, a hyphen indicates that the trait was not tested.

5.2. A comparison of morphological distances for 6 African groups.

The six largest groups were used to compare the inter-group distances derived from the male and female subsets for metric and non-metric traits. Distance matrices were derived for each of the 6 groups:

Giza	55 males	52 females
Kerma	43 males	41 females
Naqada	50 males	51 females
Sedment	39 males	29 females
Badari	36 males	22 females
Kenya	34 males	47 females

5.2.1. Generating the morphological distances.

Metric distances

Mahalanobis distances are derived using nine, seven and five variable data sets. Since some of the groups contain missing values, the means are calculated from all available data. The distance matrices for males and females are shown in tables 5.7, 5.8 and 5.9.

Non-metric distances

For each sex, Freeman-Tukey MMDs are produced using 60 traits, the left and right sides being calculated separately. Medial traits are included with both right and left sets. Further matrices are then generated using subsets of the trait battery, excluding those particular traits which the preliminary analysis marked as unreliable (see table 5.6). The palatine and maxillary tori are excluded since they were never seen in these groups, as advised by Sjøvold (1973). By excluding the non-genetic traits, those marked by GLIM as unreliable and those with high inter-worker errors, a subset of 34 traits results. If those with high inter-worker errors are included, a subset of 48 traits is available. Sex-linkage of traits does not warrant their exclusion on this occasion since the sexes are analysed separately. The distances matrices are shown in tables 5.10 to 5.15.

TABLE 5.7.

MAHALANOBIS DISTANCES (D) FOR 6 AFRICAN POPULATIONS

MALES AND FEMALES SEPARATED.

9 variables used:

GOL, BNL, XCB, ZYB, NPH, NLH, OBH, NLB, ZMB.

MALES.

Kerma	1.7036				
Naqada	1.7546	0.9695			
Sedment	1.4540	1.6094	1.8593		
Badari	2.4254	1.4108	0.8828	2.3457	
Teita	3.2622	2.3754	2.7097	3.6823	2.8734
	Giza	Kerma	Naqada	Sedment	Badari

FEMALES.

Kerma	2.2040				
Naqada	2.2071	0.8793			
Sedment	1.7085	1.7870	1.8520		
Badari	2.3648	1.1957	1.1829	1.9341	
Teita	3.9177	3.1859	3.6224	4.4219	3.8608
	Giza	Kerma	Naqada	Sedment	Badari

These values are plotted in fig. 5.1, in which the groups are identified by the following codes:

Giza - G Kerma - K Naqada - N Sedment - S Badari - B Teita - T

TABLE 5.8.

MAHALANOBIS DISTANCES (D) FOR 6 AFRICAN POPULATIONS

MALES AND FEMALES SEPARATED.

7 variables used:

BNL, ZYB, NPH, NLH, OBH, NLB, ZMB.

MALES.

Kerma	1.3957				
Naqada	1.4897	0.7879			
Sedment	1.2224	1.2931	1.3213		
Badari	1.9101	1.2031	0.6484	1.6298	
Teita	2.3504	1.9852	2.2677	2.9736	2.7186
	Giza	Kerma	Naqada	Sedment	Badari

FEMALES.

Kerma	1.7752				
Naqada	1.8875	0.7055			
Sedment	1.6014	1.1009	1.1345		
Badari	2.0728	1.1246	1.1766	1.3231	
Teita	2.5570	2.6601	2.8662	3.3987	3.2276
	Giza	Kerma	Naqada	Sedment	Badari

These values are plotted in fig. 5.2, in which the groups are identified by the following codes:

Giza - G Kerma - K Naqada - N Sedment - S Badari - B Teita - T

TABLE 5.9.

MAHALANOBIS DISTANCES (D) FOR 6 AFRICAN POPULATIONS

MALES AND FEMALES SEPARATED.

5 variables used:

GOL, XCB, NPH, OBH, NLB.

MALES.

Kerma	1.1240				
Naqada	1.1459	0.4763			
Sedment	1.2731	1.4294	1.6408		
Badari	1.8793	1.1186	0.7851	2.1558	
Teita	2.8059	1.8996	1.9614	3.2494	1.9325
	Giza	Kerma	Naqada	Sedment	Badari

FEMALES.

Kerma	1.4970				
Naqada	1.1833	0.4797			
Sedment	1.3531	1.4928	1.4371		
Badari	1.5406	1.0705	0.7284	1.6989	
Teita	3.4160	2.6727	2.8797	3.8223	3.1870
	Giza	Kerma	Naqada	Sedment	Badari

These values are plotted in fig. 5.3, in which the groups are identified by the following codes:

Giza - G Kerma - K Naqada - N Sedment - S Badari - B Teita - T

TABLE 5.10.

MMD FOR 6 POPULATIONS : MALES AND FEMALES.

LEFT side only used for bilateral traits.

34 traits used: 2, 4-7, 9-10, 14, 16-21, 25, 26, 29-31, 36, 39-41, 44, 46, 48, 50, 52-57, 60.

MALES.

Kerma	0.0085 0.0106		Upper figure Lower figure *	- Freeman-Tukey MMD - St. error of MMD - MMD significant. ($p < 0.05$)	
Naqada	-0.0004 0.0097	0.0054 0.0112			
Sedment	0.0001 0.0112	-0.0054 0.0128	-0.0120 0.0119		
Badari	0.0088 0.0121	0.0278* 0.0137	-0.0175 0.0127	-0.0157 0.0143	
Teita	0.0195 0.0121	0.0013 0.0136	-0.0051 0.0127	0.0012 0.0143	-0.0010 0.0151
	Giza	Kerma	Naqada	Sedment	Badari

FEMALES.

Kerma	0.0252* 0.0110				
Naqada	-0.0046 0.0097	-0.0015 0.0112			
Sedment	0.0107 0.0137	0.0118 0.0152	0.0167* 0.0139		
Badari	0.0150 0.0179	0.0184 0.0194	0.0397 0.0181	-0.0200 0.0221	
Teita	0.0253* 0.0104	0.0164 0.0119	0.0137 0.0106	0.0180 0.0146	0.0116 0.0188
	Giza	Kerma	Naqada	Sedment	Badari

These values are plotted in fig. 5.4, in which the groups are identified by the following codes:

Giza - G Kerma - K Naqada - N Sedment - S Badari - B Teita - T

TABLE 5.11.

MMD FOR 6 POPULATIONS : MALES AND FEMALES.

RIGHT side only used for bilateral traits.

34 traits used: 2, 4-7, 9-10, 14, 16-21, 25, 26, 29-31,
36, 39-41, 44, 46, 48, 50, 52-57, 60.

MALES.

Kerma	0.0099 0.0104		Upper figure Lower figure *	- Freeman-Tukey MMD - St. error of MMD - MMD significant. ($p < 0.05$)	
Naqada	0.0097 0.0095	0.0249* 0.0109			
Sedment	0.0152 0.0111	0.0320* 0.0125	0.0111 0.0116		
Badari	0.0156 0.0121	0.0349* 0.0135	-0.0125 0.0127	0.0113 0.0143	
Teita	-0.0112 0.0120	-0.0187 0.0134	-0.0065 0.0125	0.0026 0.0141	-0.0209 0.0152
	Giza	Kerma	Naqada	Sedment	Badari

FEMALES.

Kerma	0.0233* 0.0113				
Naqada	-0.0029 0.0098	-0.0030 0.0114			
Sedment	0.0092 0.0137	0.0518* 0.0153	0.0069 0.0138		
Badari	0.0016 0.0184	0.0201 0.0199	-0.0009 0.0185	-0.0032 0.0224	
Teita	0.0379* 0.0105	0.0507* 0.0120	0.0117 0.0106	0.0085 0.0145	0.0217 0.0191
	Giza	Kerma	Naqada	Sedment	Badari

These values are plotted in fig. 5.5, in which the groups are identified by the following codes:

Giza - G Kerma - K Naqada - N Sedment - S Badari - B Teita - T

TABLE 5.12.

MMD FOR 6 POPULATIONS : MALES AND FEMALES.

LEFT side only used for bilateral traits.

48 traits used: 1, 2, 4-7, 9-10, 14-21, 25, 26, 28-34, 36-41, 44-60

MALES.

Kerma	0.0150 0.0089				
Naqada	0.0067 0.0081	0.0199* 0.0095			
Sedment	-0.0043 0.0095	0.0102 0.0109	0.0068 0.0101		
Badari	0.0050 0.0104	0.0460* 0.0117	-0.0064 0.0110	-0.0145 0.0124	
Teita	0.0295* 0.0102	0.0132 0.0116	0.0280* 0.0108	0.0248* 0.0122	0.0183 0.0131
	Giza	Kerma	Naqada	Sedment	Badari

Upper figure - Freeman-Tukey MMD
Lower figure - St. error of MMD
* - MMD significant. ($p < 0.05$)

FEMALES.

Kerma	0.0318* 0.0092				
Naqada	0.0021 0.0082	0.0134 0.0094			
Sedment	0.0143 0.0116	0.0336* 0.0129	0.0353* 0.0118		
Badari	0.0138 0.0154	0.0091 0.0167	0.0373* 0.0156	-0.0088 0.0191	
Teita	0.0602* 0.0087	0.0314* 0.0100	0.0522* 0.0089	0.0807* 0.0124	0.0465* 0.0162
	Giza	Kerma	Naqada	Sedment	Badari

These values are plotted in fig. 5.6, in which the groups are identified by the following codes:

Giza - G Kerma - K Naqada - N Sedment - S Badari - B Teita - T

TABLE 5.13.

MMD FOR 6 POPULATIONS : MALES AND FEMALES.

RIGHT side only used for bilateral traits.

48 traits used: 1, 2, 4-7, 9-10, 14-21, 25, 26, 28-34, 36-41, 44-60

MALES.

Kerma	0.0075 0.0087		Upper figure Lower figure *	- Freeman-Tukey MMD - St. error of MMD - MMD significant. ($p < 0.05$)	
Naqada	0.0139 0.0081	0.0345* 0.0093			
Sedment	0.0072 0.0094	0.0228* 0.0106	0.0034 0.0100		
Badari	0.0186 0.0105	0.0367* 0.0117	-0.0140 0.0111	0.0021 0.0123	
Sedment	0.0106 0.0102	0.0044 0.0114	0.0289* 0.0108	0.0202 0.0120	0.0017 0.0131
	Giza	Kerma	Naqada	Sedment	Badari

FEMALES.

Kerma	0.0409* 0.0094				
Naqada	-0.0008 0.0082	0.0120 0.0096			
Sedment	0.0279* 0.0116	0.0756* 0.0129	0.0213 0.0117		
Badari	-0.0030 0.0161	0.0147 0.0174	-0.0031 0.0163	0.0275 0.0196	
Sedment	0.0726* 0.0087	0.0550* 0.0100	0.0405* 0.0089	0.0883* 0.0122	0.0461* 0.0168
	Giza	Kerma	Naqada	Sedment	Badari

These values are plotted in fig. 5.7, in which the groups are identified by the following codes:

Giza - G Kerma - K Naqada - N Sedment - S Badari - B Teita - T

TABLE 5.14.

MMD FOR 6 POPULATIONS : MALES AND FEMALES.

LEFT side only used for bilateral traits.

All 60 traits used

MALES.

Kerma	0.0131 0.0079		Upper figure Lower figure *	- Freeman-Tukey MMD - St. error of MMD - MMD significant. ($p < 0.05$)	
Naqada	0.0070 0.0072	0.0145 0.0084			
Sedment	-0.0020 0.0084	0.0069 0.0096	-0.0003 0.0089		
Badari	0.0026 0.0091	0.0338* 0.0103	-0.0125 0.0097	-0.0175 0.0109	
Teita	0.0433* 0.0091	0.0184 0.0102	0.0257* 0.0096	0.0235* 0.0108	0.0209 0.0115
	Giza	Kerma	Naqada	Sedment	Badari

FEMALES.

Kerma	0.0227* 0.0082				
Naqada	0.0006 0.0073	0.0091 0.0084			
Sedment	0.0294* 0.0103	0.0303* 0.0114	0.0406* 0.0105		
Badari	0.0177 0.0136	0.0001 0.0147	0.0291* 0.0138	-0.0176 0.0168	
Teita	0.0506* 0.0077	0.0253* 0.0088	0.0503* 0.0079	0.0662* 0.0109	0.0373* 0.0143
	Giza	Kerma	Naqada	Sedment	Badari

These values are plotted in fig. 5.8, in which the groups are identified by the following codes:

Giza - G Kerma - K Naqada - N Sedment - S Badari - B Teita - T

TABLE 5.15.

MMD FOR 6 POPULATIONS : MALES AND FEMALES.

RIGHT side only used for bilateral traits.

All 60 traits used.

MALES.

Kerma	0.0136 0.0078		Upper figure Lower figure *	- Freeman-Tukey MMD - St. error of MMD - MMD significant. ($p < 0.05$)	
Naqada	0.0110* 0.0072	0.0309* 0.0082			
Sedment	0.0095 0.0083	0.0268* 0.0094	-0.0043 0.0088		
Badari	0.0231* 0.0092	0.0415* 0.0103	-0.0102 0.0097	0.0013 0.0108	
Teita	0.0270* 0.0090	0.0111 0.0101	0.0331* 0.0095	0.0301* 0.0107	0.0318* 0.0116
	Giza	Kerma	Naqada	Sedment	Badari

FEMALES.

Kerma	0.0340* 0.0083				
Naqada	-0.0003 0.0073	0.0154 0.0084			
Sedment	0.0319* 0.0103	0.0611* 0.0114	0.0185 0.0104		
Badari	-0.0095 0.0141	0.0039 0.0152	-0.0099 0.0142	0.0160 0.0172	
Teita	0.0577* 0.0077	0.0455* 0.0089	0.0374* 0.0078	0.0762* 0.0108	0.0348* 0.0147
	Giza	Kerma	Naqada	Sedment	Badari

These values are plotted in fig. 5.9, in which the groups are identified by the following codes:

Giza - G Kerma - K Naqada - N Sedment - S Badari - B Teita - T

5.2.2. Multidimensional scaling.

All distance matrices are converted to coordinate points using the MDS(X) program MINISSA. The scaling program revealed that nothing is gained by using more than three dimensions. All metric distance matrices can also be adequately described in two dimensions. The non-metric matrices are all adequately portrayed in three dimensions; they can also be portrayed in two-dimensions, though some of these show unacceptably high stress coefficients. A three-dimensional solution is therefore chosen for all the matrices, since a plot in this number of dimensions can be examined visually, and comparison of the coordinates is simplified if all plots have the same dimensionality. The plots of the co-ordinate points are shown in figs 5.1 to 5.9. The relational aspect of these plots, as evidenced by a visual examination will be considered later.

5.2.3. Procrustes analysis.

Table 5.16 shows the results of comparing the distance matrices for:

1. Metric variates: male vs. female
2 Non-metric traits: male vs. female
3. Non-metric traits: left side vs. right side
4. Metric variates: different sets of measurements
5. Non-metric traits: different sets of traits.
6. Metric variates vs. non-metric traits.

The R^2 values indicate the degree of correspondance between the plots, where a value of 0 represents perfect correspondence and 1 maximum dissimilarity.

5.2.4. Summary

It is apparent that there is very good agreement, as shown by the low R^2 values (mean of 3 R^2=0.099, range 0.048-0.176) between the interpopulation distances derived from male and female metric traits. There is much less agreement between male and female distances for non-metric trait based distances (mean of 6 R^2=0.522, range 0.292-0.683). Similarly, the agreement between MMDs based on left and right sides (mean of 6 R^2 =0.263, range 0.091-0.384) is poorer than expected.

Non-specificity (Sokal and Sneath 1963), as shown in comparisons of different sets of variates, is slightly greater for metric (mean R^2 of 6 values = 0.155, range 0.067-0.251) than

for non-metric (mean R^2 of 12 values = 0.217, range 0.008-0.540) traits. It is interesting that for metric traits, plots derived from male crania are more congruent than those derived from females (mean value of R^2=0.095 for males, 0.214 for females), and that this trend is reversed for non-metric traits (male mean R^2=0.313, female mean R^2=0.121), though the meaning of this trend is not clear. Finally, comparisons of metric and non-metric distances in both the sexes reveal that there is little correspondance between metric and epigenetic distance matrices (mean of 12 R^2=0.434, range 0.301-0.578). Cheverud Buikstra and Twichell (1979) and Corruccini (1976) found significant correlation between metric and non-metric traits, but the results obtained here do not suggest that both trait-types are equivalent reflections of the genome.

Population relationships of the Ancient Egyptians and the Teita.

Examination of the metric plots (figs. 5.1-5.3) shows that all emphasise the distinctiveness of the Teita crania; the similarity of Badari and Naqada (the two predynastic sites) and show some affinity between Sedment and Giza. Kerma most often appears near the predynastic sites. The relationships revealed by the non-metric plots (figs. 5.4-5.9) are more obscure. The distinctiveness of the Teita only becomes apparent as the number of traits employed increases, and Kerma is shown either as distinct from all other groups or, forming a separate cluster with the Teita.

It might be argued that plots do not fully exploit the information contained in MMD values, since there is no distinction made between significant and non-significant distances. Most non-metric studies have relied on a visual inspection of the matrices, but even this method reveals glaring discrepancies. If negative values are interpreted to mean that there is no distinction between the groups, many of the matrices show no distinction between the Teita and the Egyptian groups. Also males from Naqada and Sedment are often indistinguishable, while the females are significantly distinct. Inconsistencies are more common as fewer variables are employed, yet the preliminary analysis showed that nearly half of the traits violated the mathematical assumptions of the MMD formula. It appears that errors arising because the trait battery is too small exceed the errors entailed in using unreliable traits.

TABLE 5.16

COMPARISON OF PAIRS OF DISTANCE MATRICES FOR 6 AFRICAN GROUPS

(USING PROCRUSTES ANALYSIS OF 3-DIMENSIONAL COORDINATES)

Pairs compared		R2 (residual variance)
METRIC		
Males vs. Females		
	9 variate	0.074
	7 variate	0.176
	5 variate	0.048
NON-METRIC		
Males vs. Females.		
	34 traits - Left	0.422
	34 traits - Right	0.619
	48 traits - Left	0.292
	48 traits - Right	0.683
	60 traits - Left	0.585
	60 traits - Right	0.530
Left vs. Right Side		
	34 traits - male	0.384
	34 traits - female	0.200
	48 traits - male	0.319
	48 traits - female	0.349
	60 traits - male	0.091
	60 traits - female	0.235

TABLE 5.16 CONTINUED

COMPARISON OF PAIRS OF DISTANCE MATRICES FOR 6 AFRICAN GROUPS

(USING PROCRUSTES ANALYSIS OF 3-DIMENSIONAL COORDINATES)

Pairs compared		R2 (residual variance)
METRIC		
Different sets of variates		
	9 vs.7 males	0.089
	9 vs.7 females	0.234
	9 vs.5 males	0.067
	9 vs.5 females	0.158
	7 vs.5 males	0.129
	7 vs.5 females	0.251
NON-METRIC		
Different sets of traits		
	34 vs.48 L male	0.366
	34 vs.48 L female	0.101
	34 vs.48 R male	0.354
	34 vs.48 R female	0.203
	34 vs.60 L male	0.218
	34 vs.60 L female	0.141
	34 vs.60 R male	0.540
	34 vs.60 R female	0.212
	48 vs.60 L male	0.199
	48 vs.60 L female	0.063
	48 vs.60 R male	0.200
	48 vs.60 R female	0.008

TABLE 5.16 CONTINUED

COMPARISON OF PAIRS OF DISTANCE MATRICES FOR 6 AFRICAN GROUPS

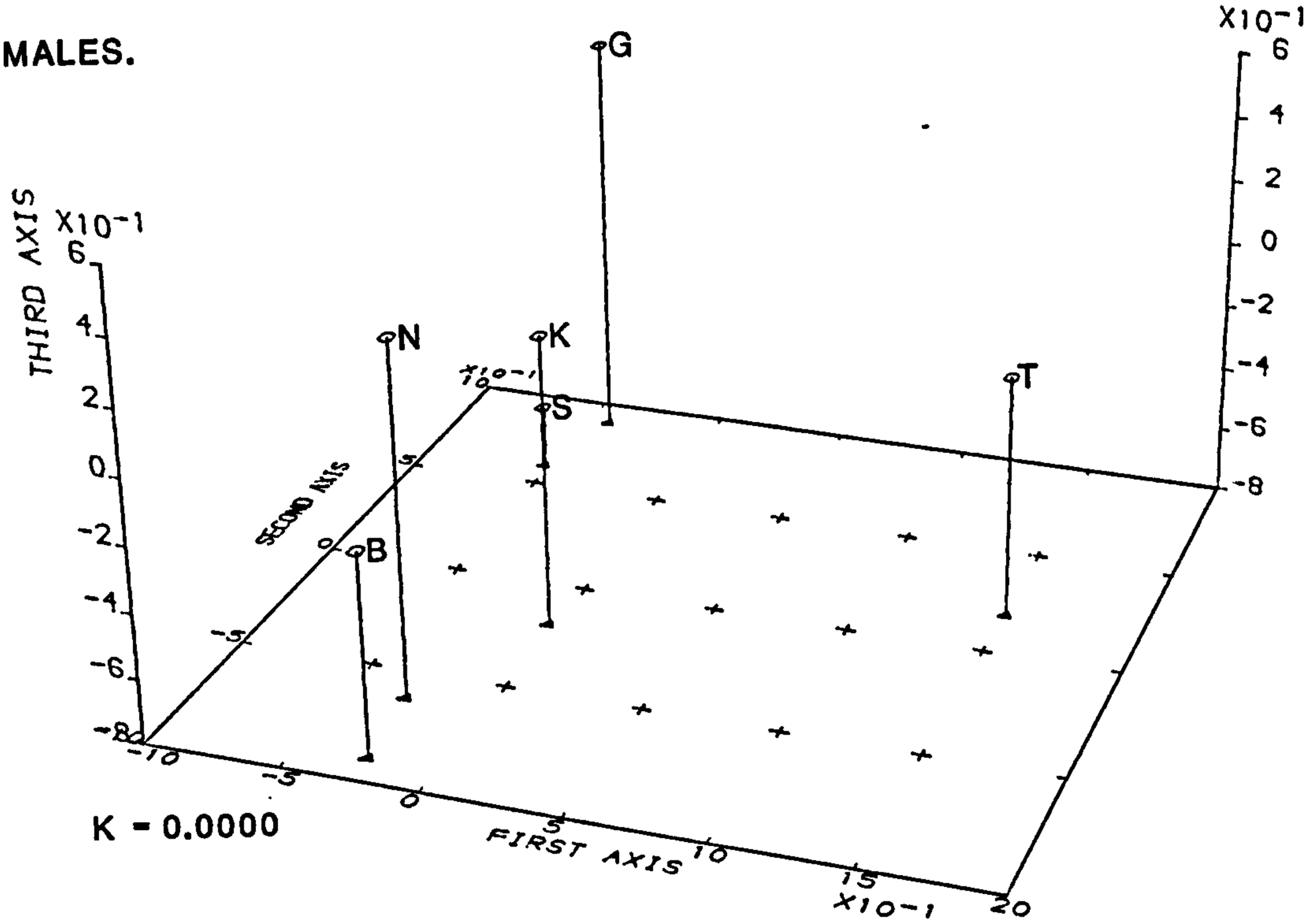
(USING PROCRUSTES ANALYSIS OF 3-DIMENSIONAL COORDINATES)

Pairs compared	R2 (residual variance)
METRIC vs. NON-METRIC (Metric based on 9 variates)	
Different sets of traits	
metric vs. 34 L male	0.443
metric vs. 34 L female	0.420
metric vs. 34 R male	0.578
metric vs. 34 R female	0.351
metric vs. 48 L male	0.516
metric vs. 48 L female	0.455
metric vs. 48 R male	0.381
metric vs. 48 R female	0.443
metric vs. 60 L male	0.450
metric vs. 60 L female	0.301
metric vs. 60 R male	0.403
metric vs. 60 R female	0.464

Fig. 5.1 Minissa plots in 3 dimensions of 6 African groups.

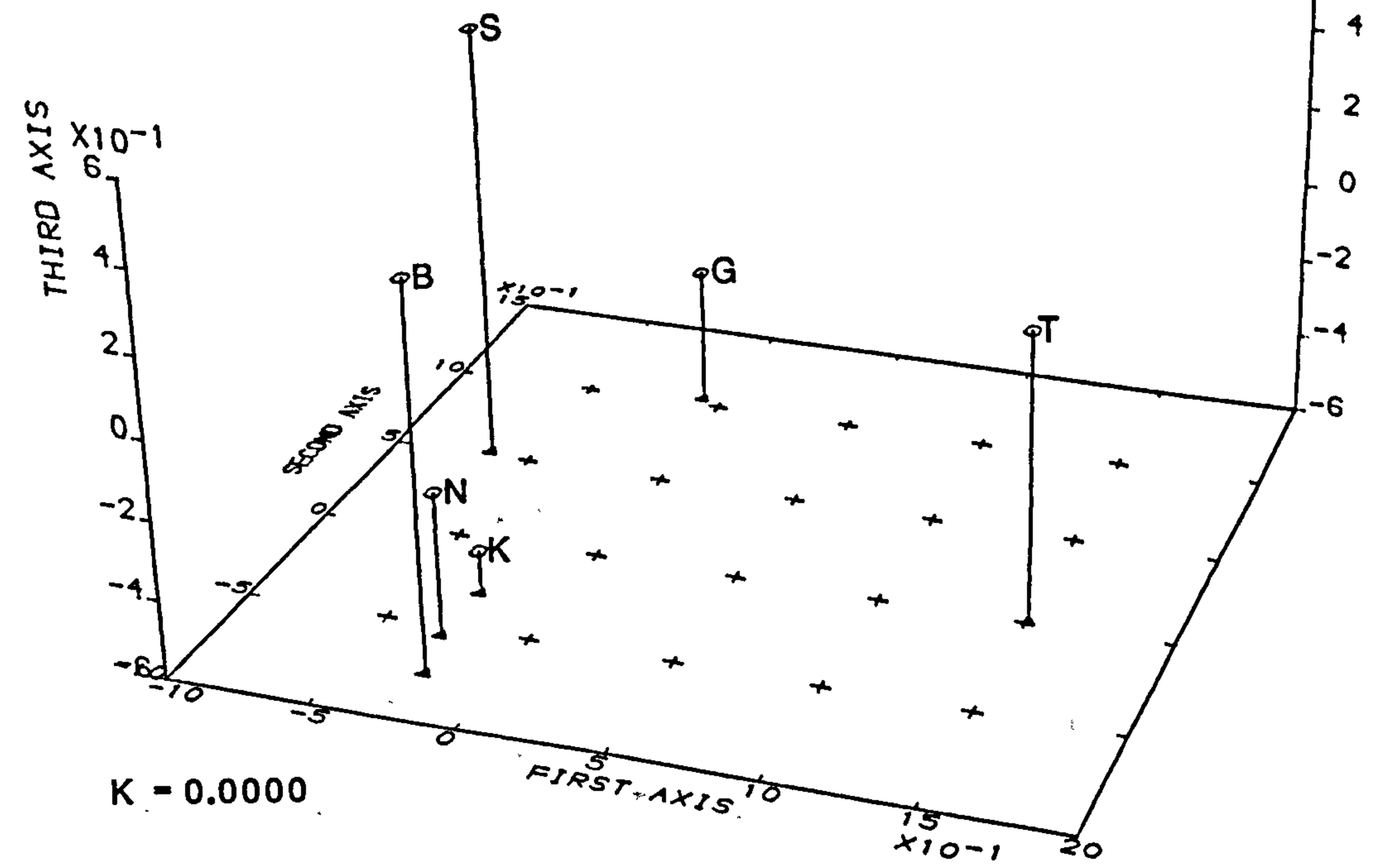
Distances derived from 9 metric traits.

MALES.



K = 0.0000

FEMALES.

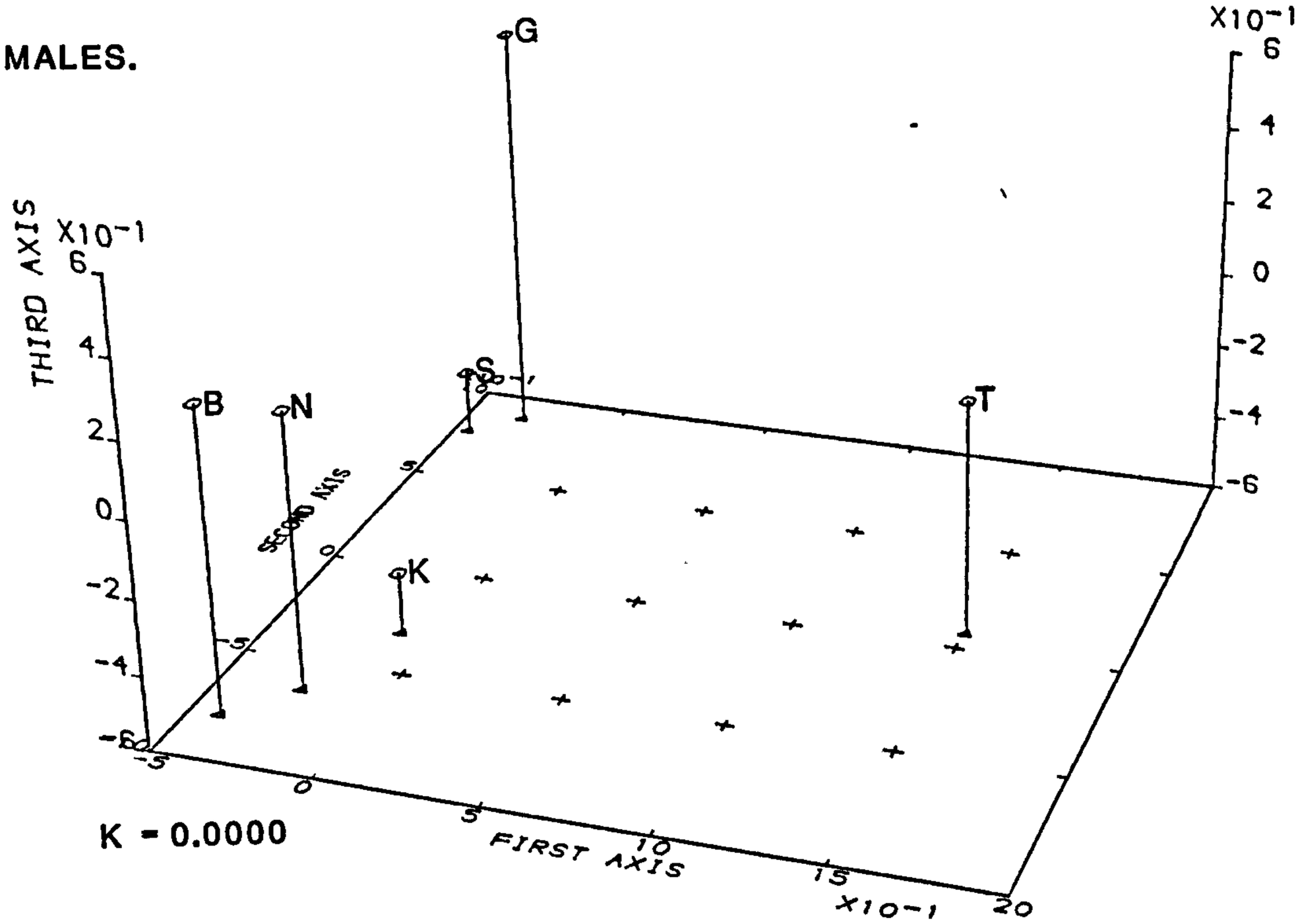


K = 0.0000

Fig. 5.2 Minissa plots in 3 dimensions of 6 African groups.

Distances derived from 7 metric traits.

MALES.



FEMALES.

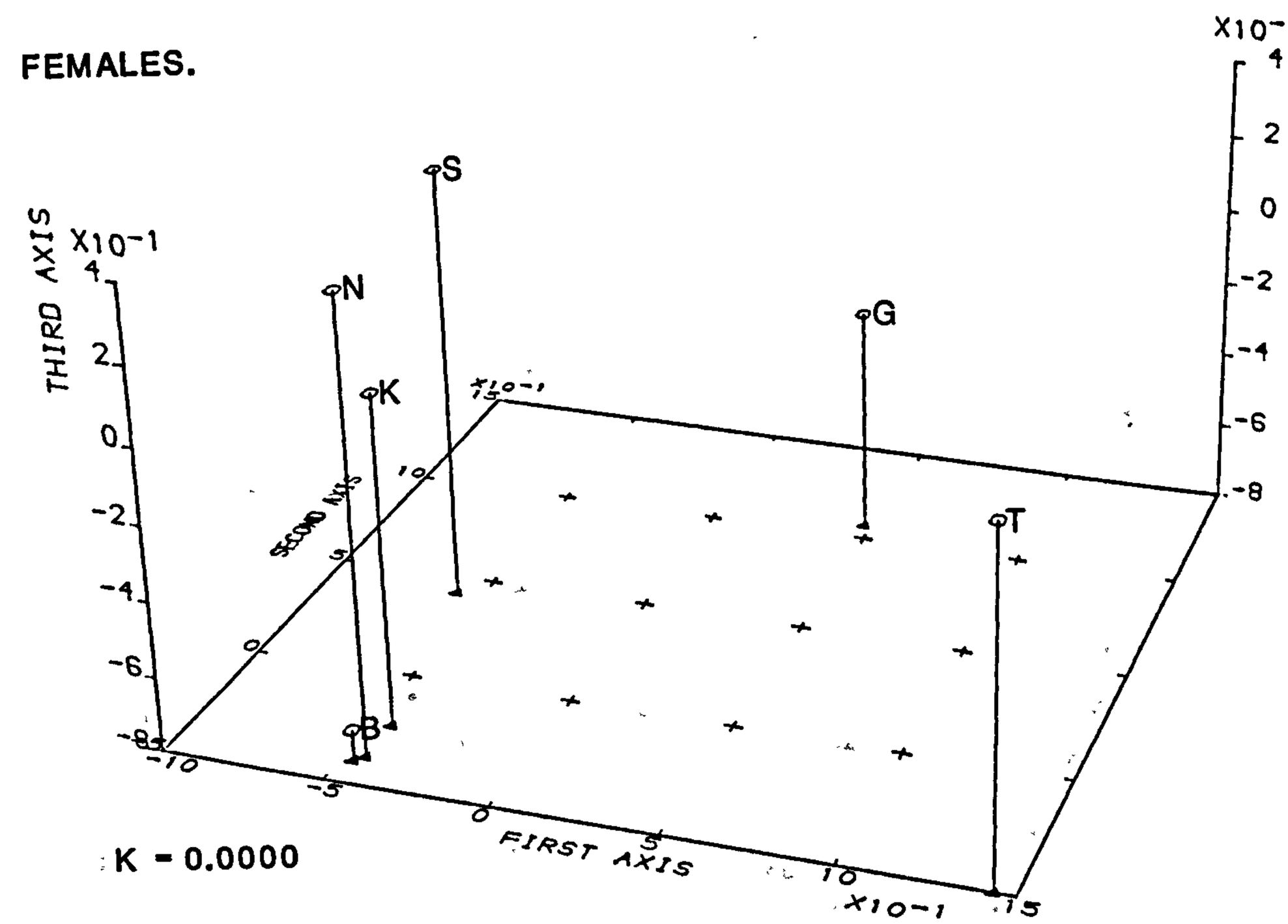
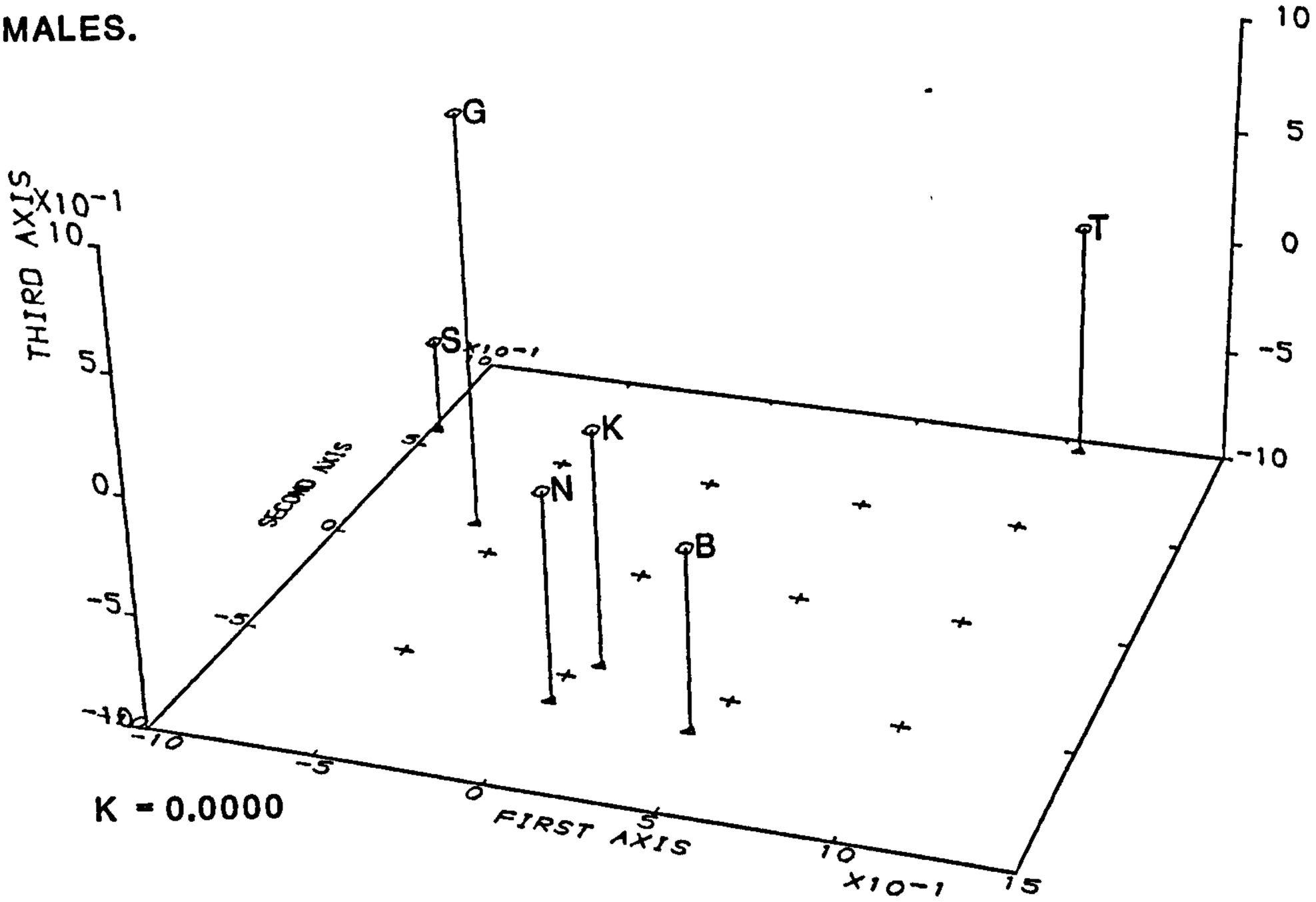


Fig. 5.3 Minissa plots in 3 dimensions of 6 African groups.

Distances derived from 5 metric traits.

MALES.



FEMALES.

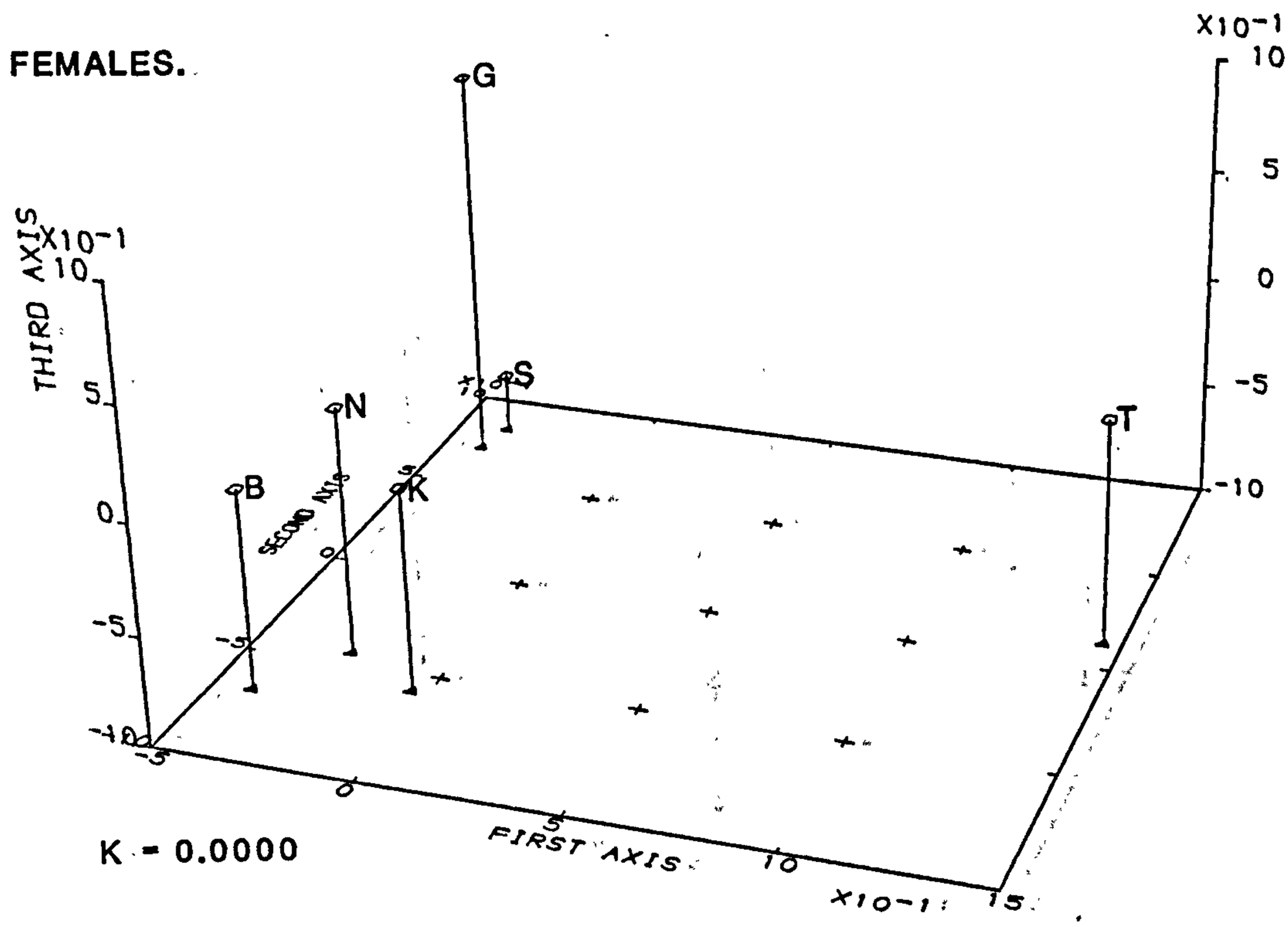
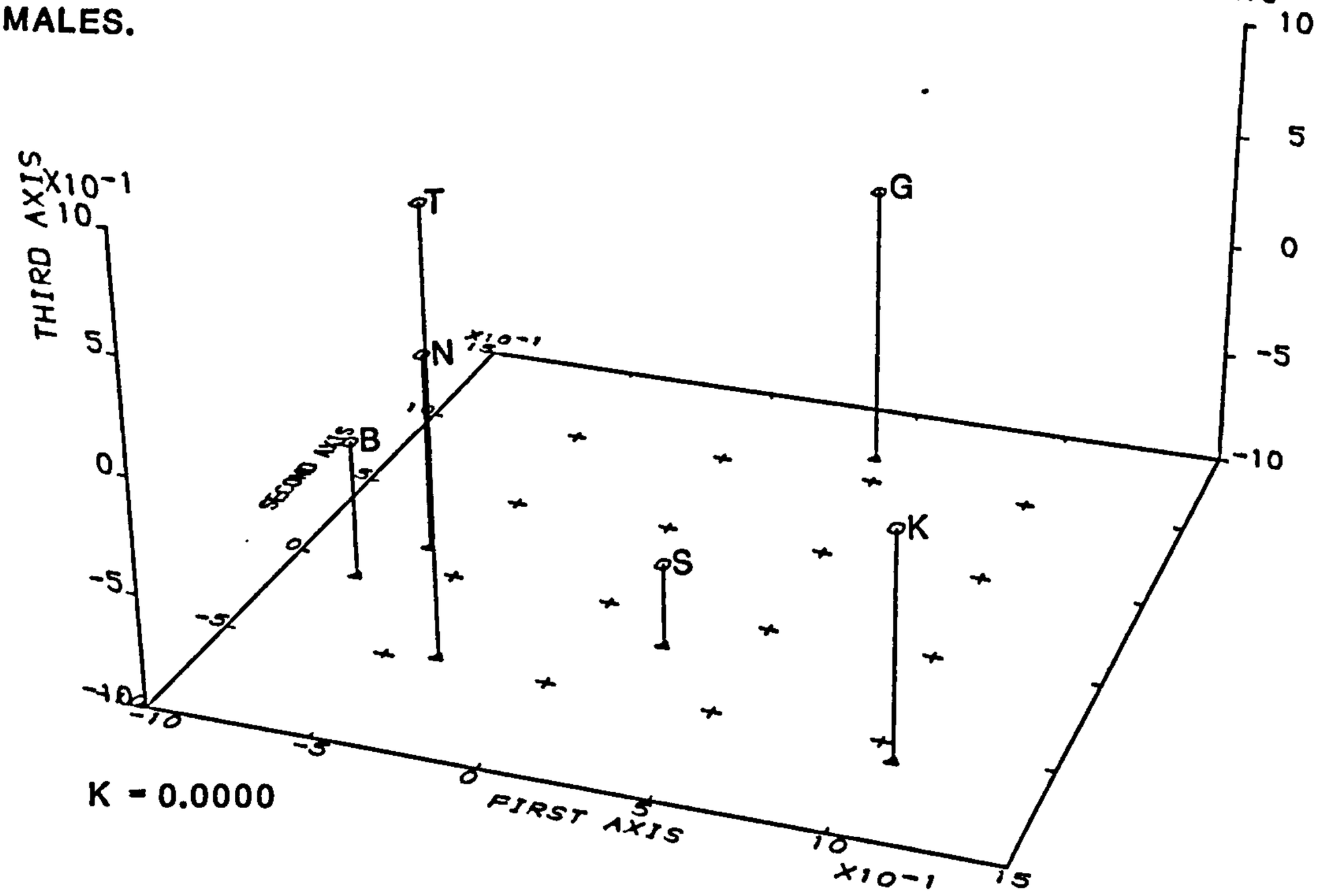


Fig. 5.4 Minissa plots in 3 dimensions of 6 African groups.

Distances derived from 34 non-metric traits.

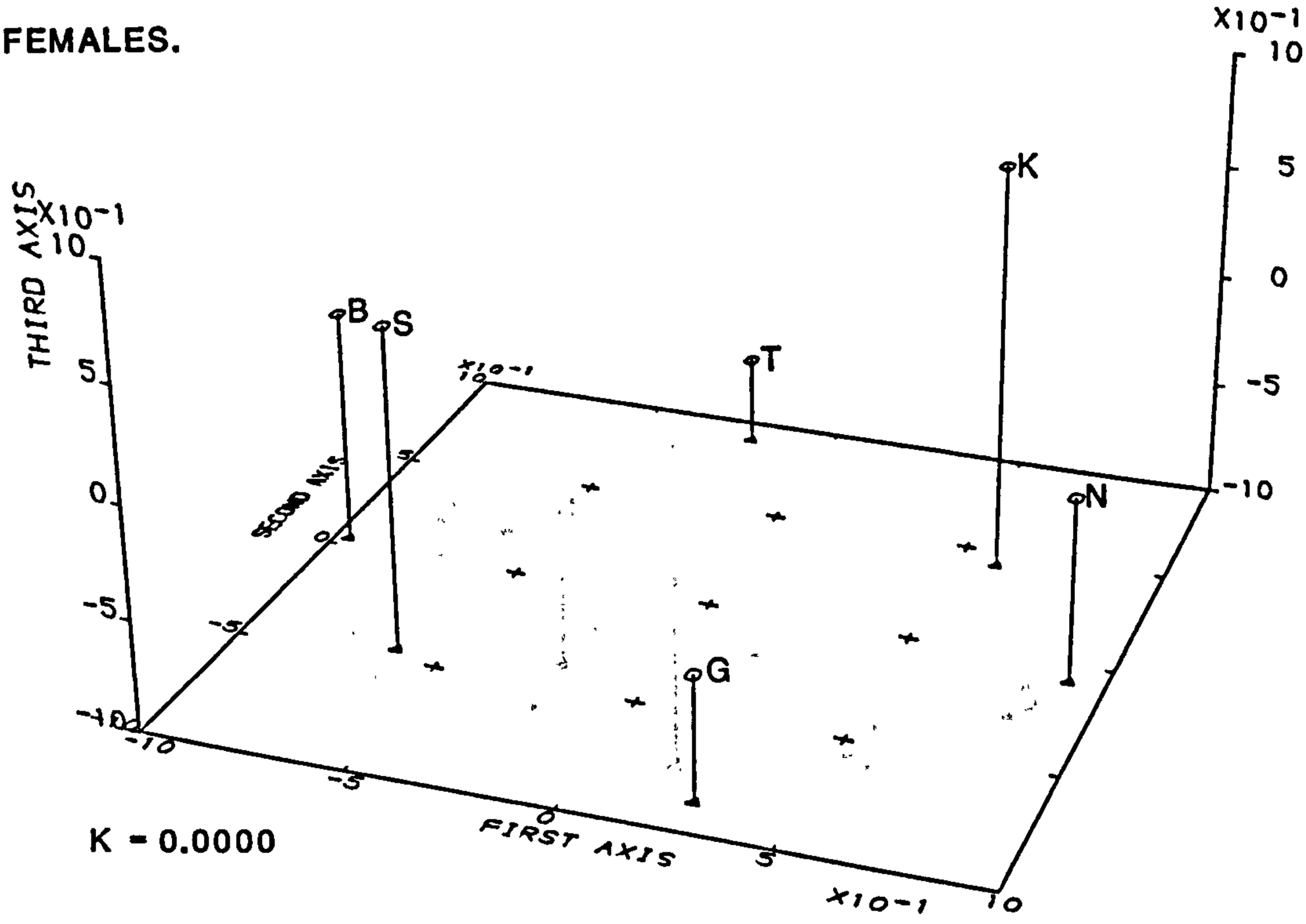
LEFT SIDE.

MALES.



K = 0.0000

FEMALES.



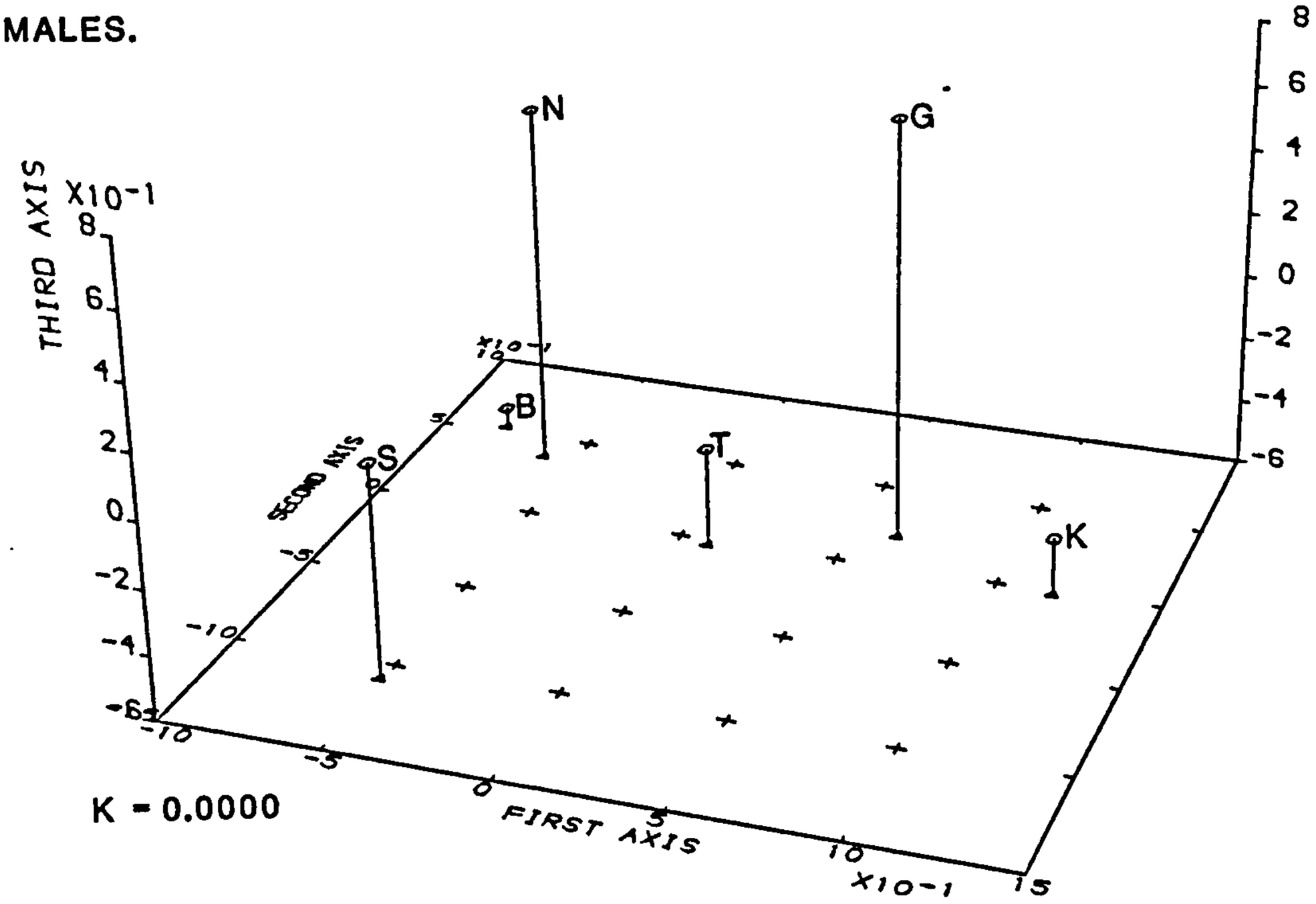
K = 0.0000

Fig. 5.5 Minissa plots in 3 dimensions of 6 African groups.

Distances derived from 34 non-metric traits.

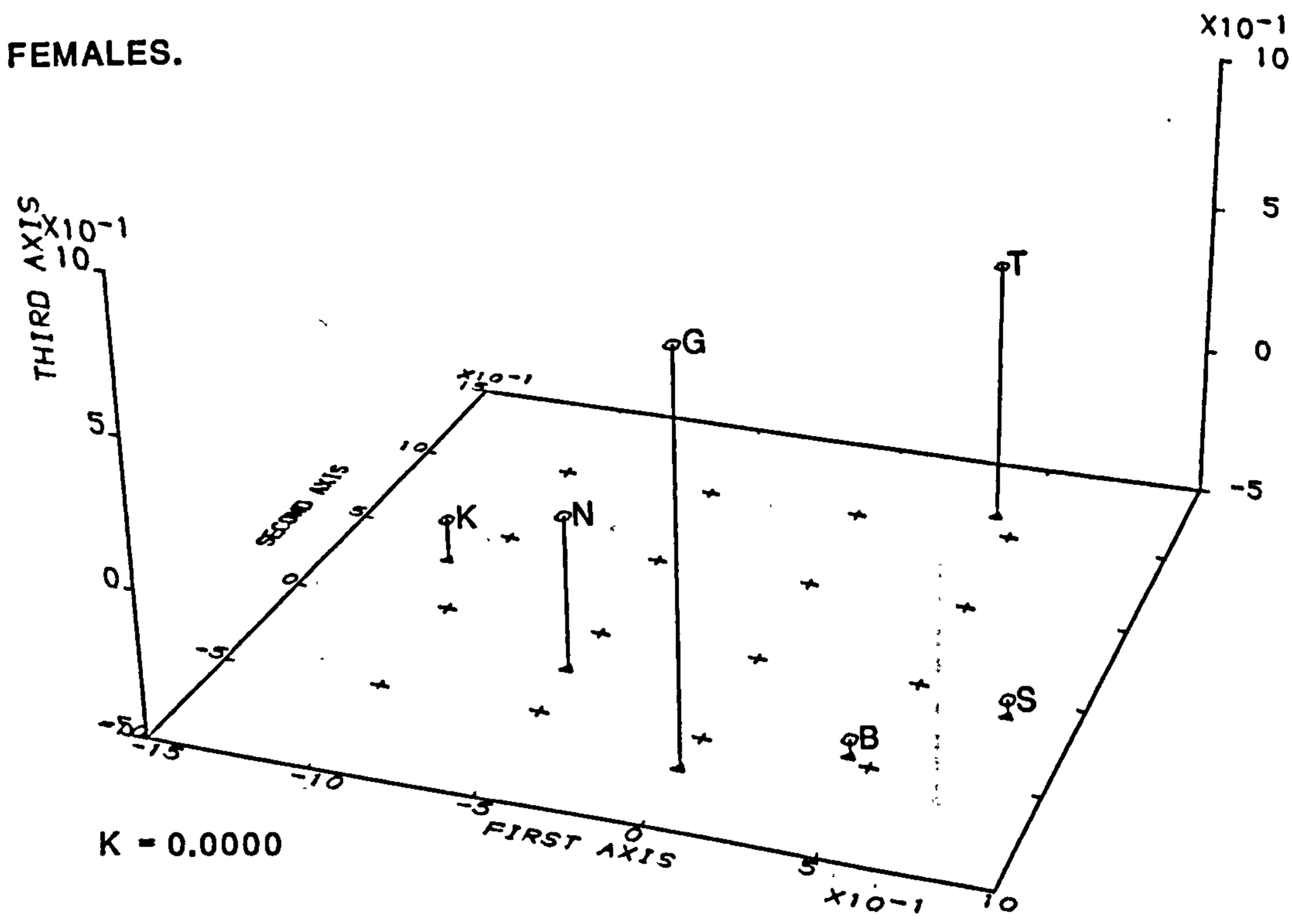
RIGHT SIDE.

MALES.



K = 0.0000

FEMALES.



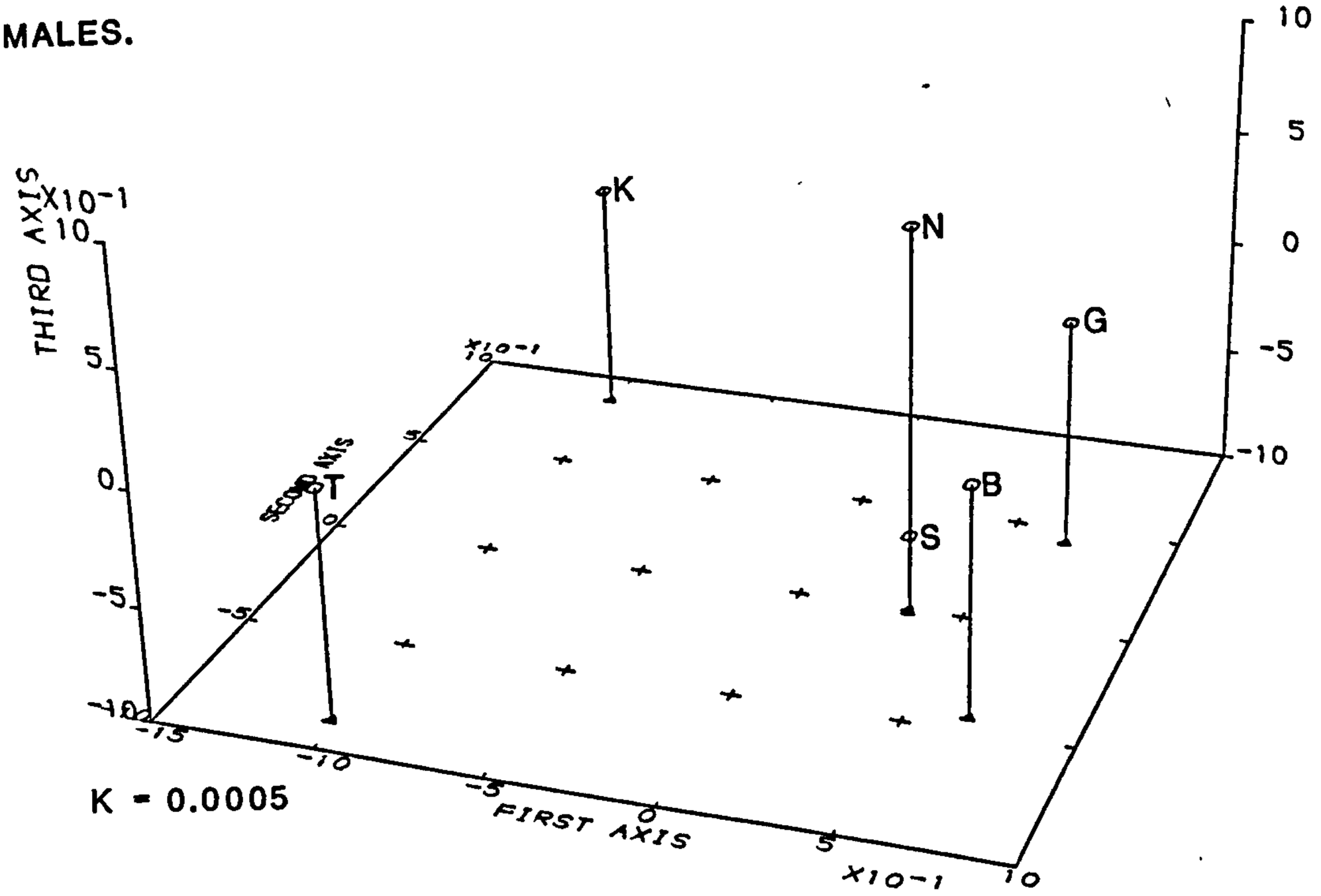
K = 0.0000

Fig. 5.6 Minissa plots in 3 dimensions of 6 African groups.

Distances derived from 48 non-metric traits.

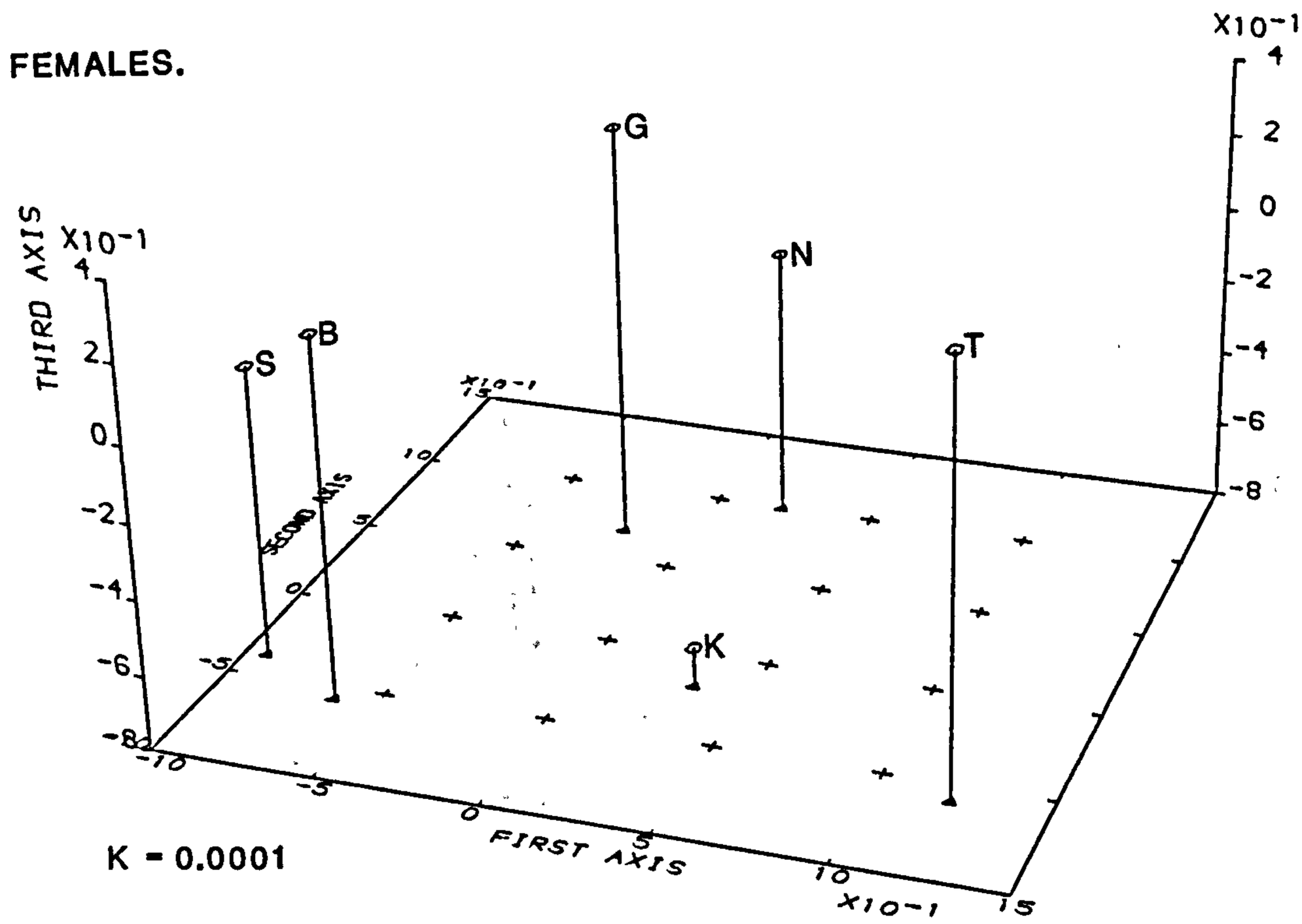
LEFT SIDE.

MALES.



K = 0.0005

FEMALES.



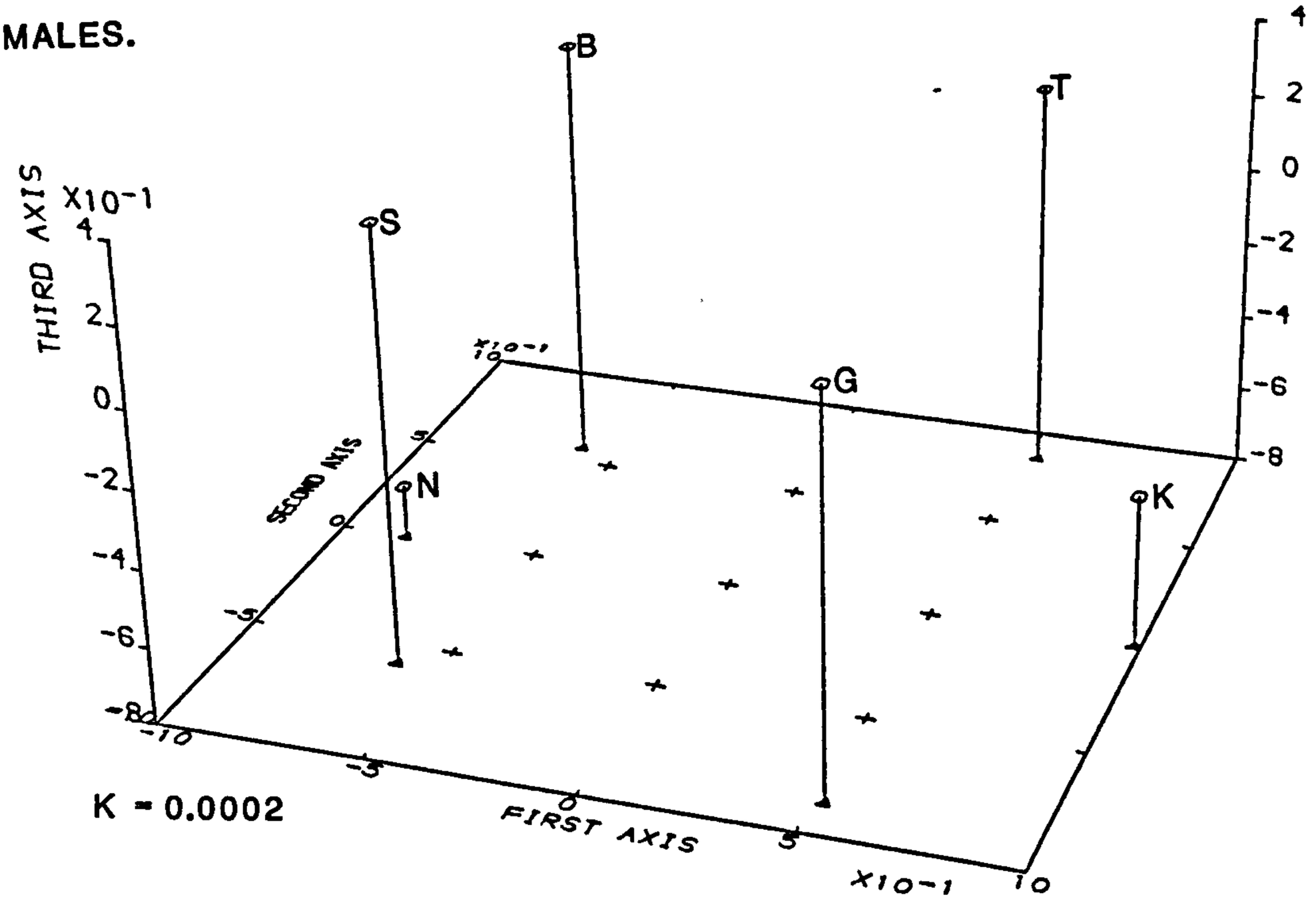
K = 0.0001

Fig. 5.7 Minissa plots in 3 dimensions of 6 African groups.

Distances derived from 48 non-metric traits.

RIGHT SIDE.

MALES.



FEMALES.

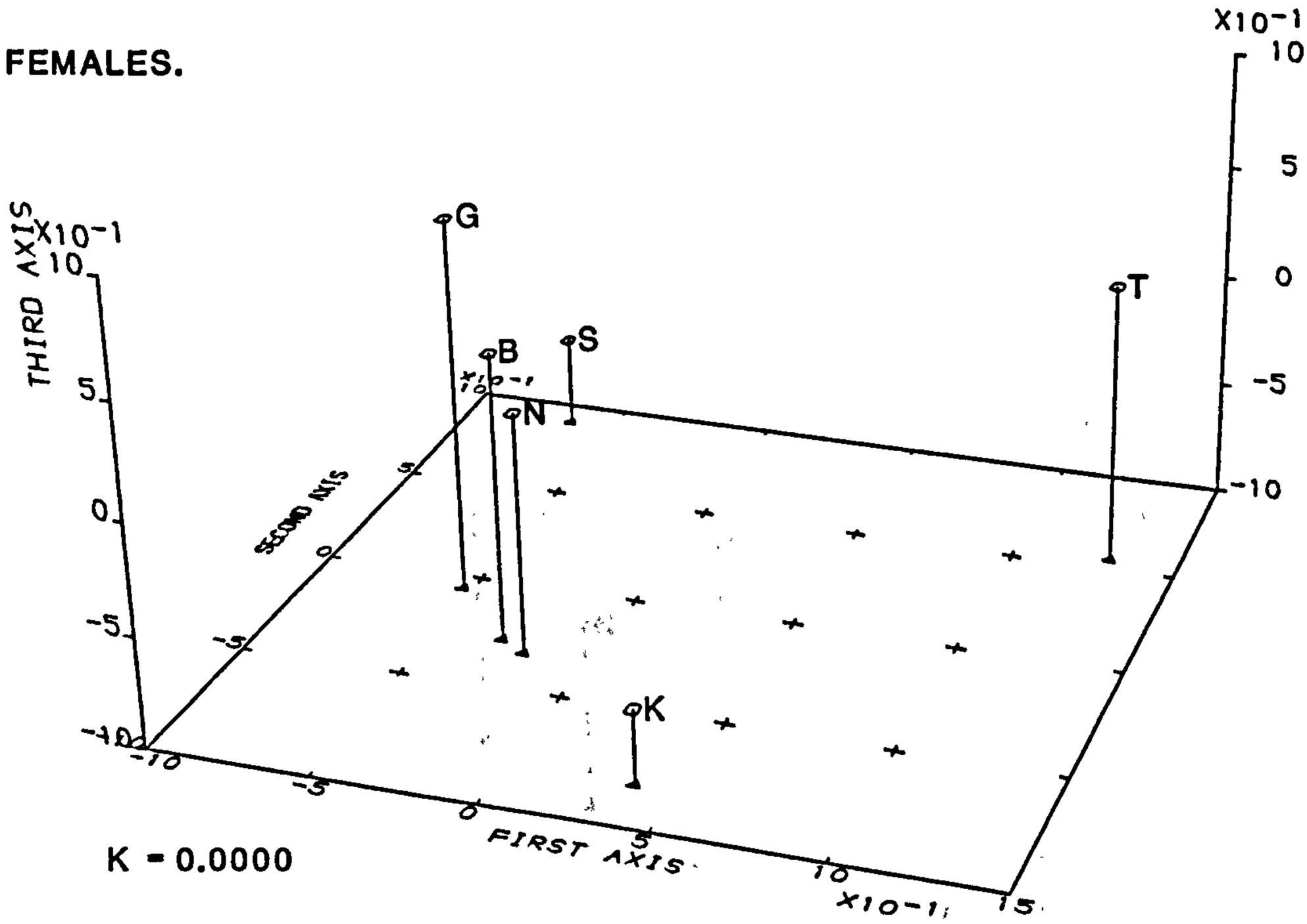
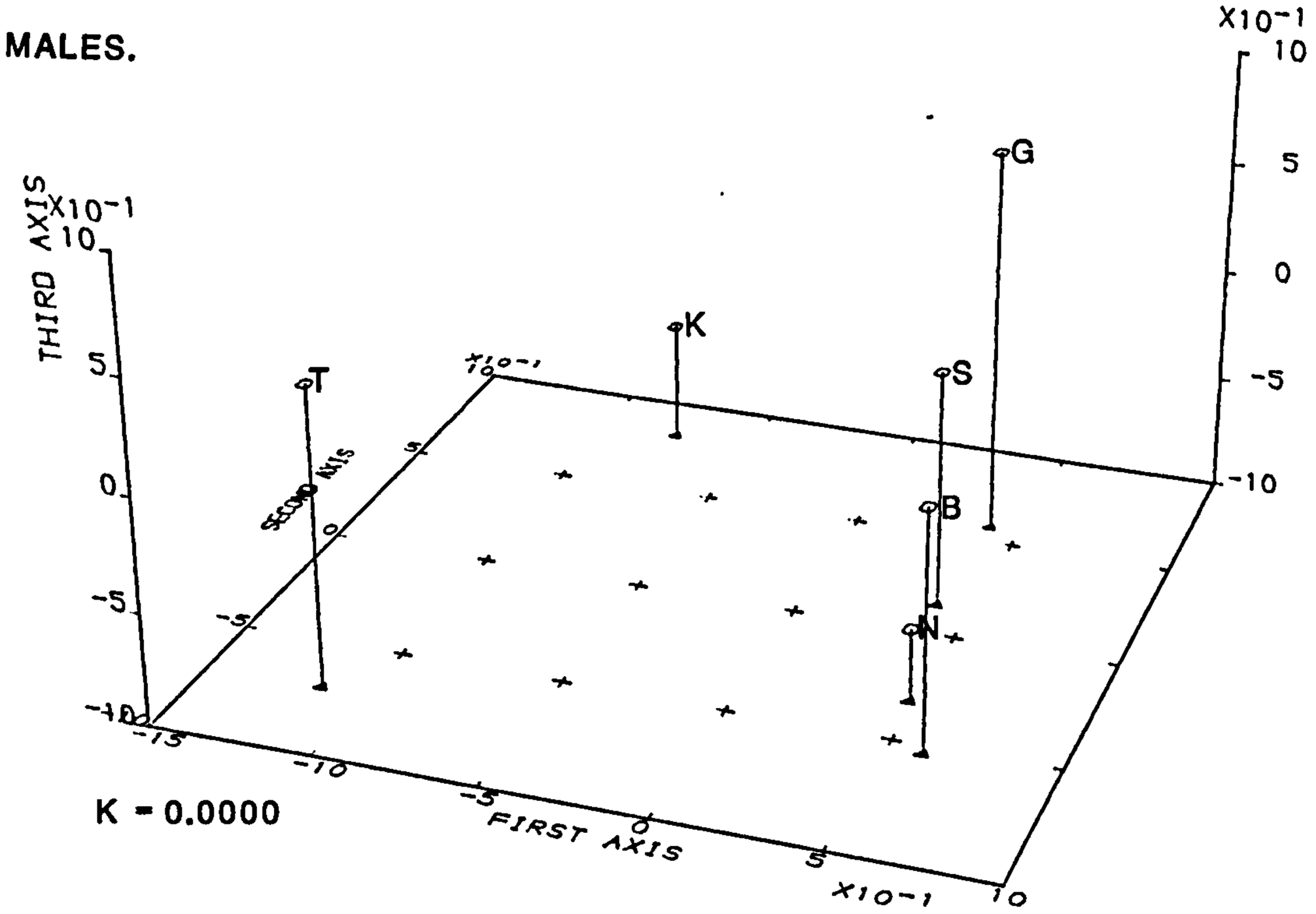


Fig. 5.8 Minissa plots in 3 dimensions of 6 African groups.

Distances derived from 60 non-metric traits.

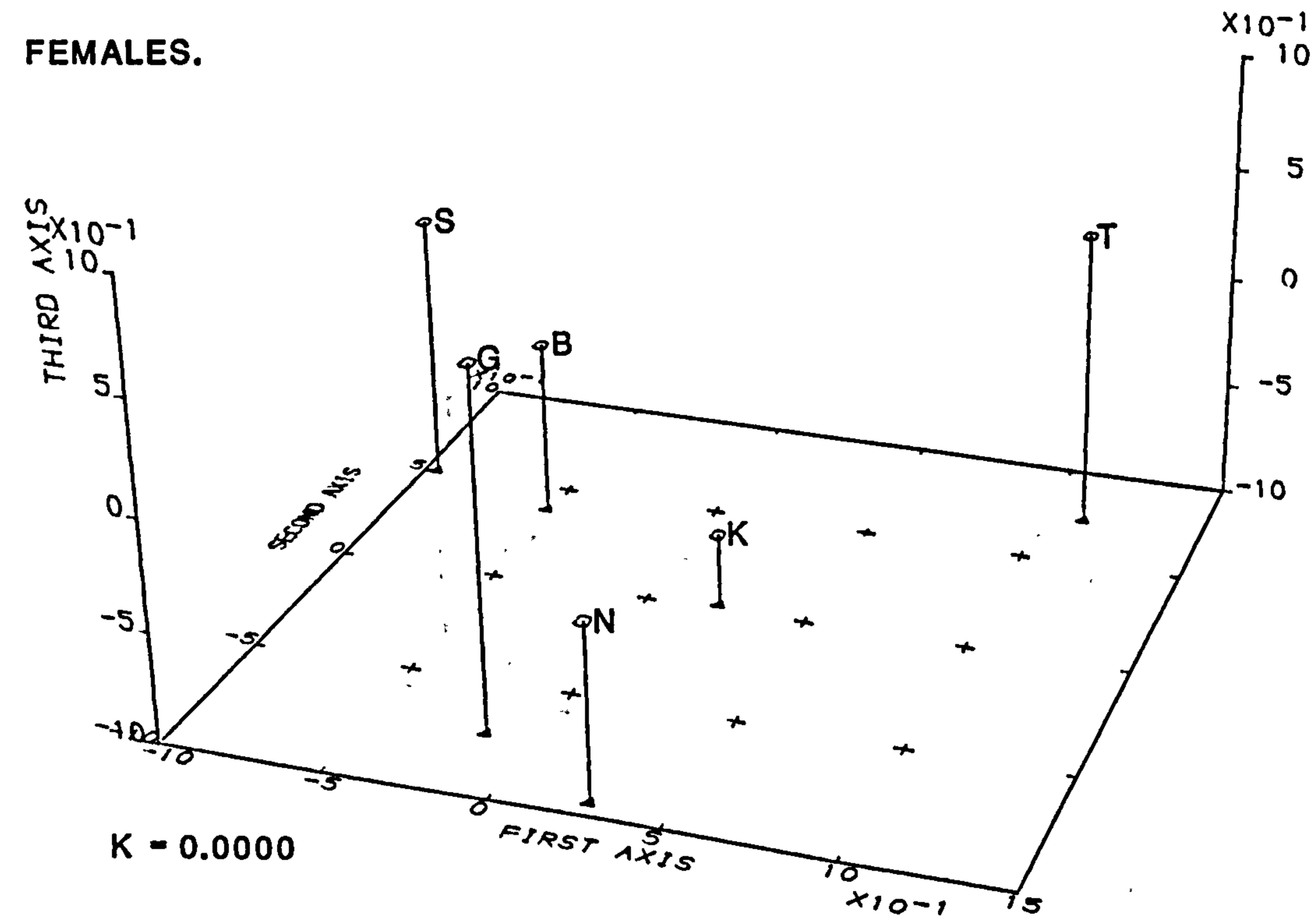
LEFT SIDE.

MALES.



K = 0.0000

FEMALES.



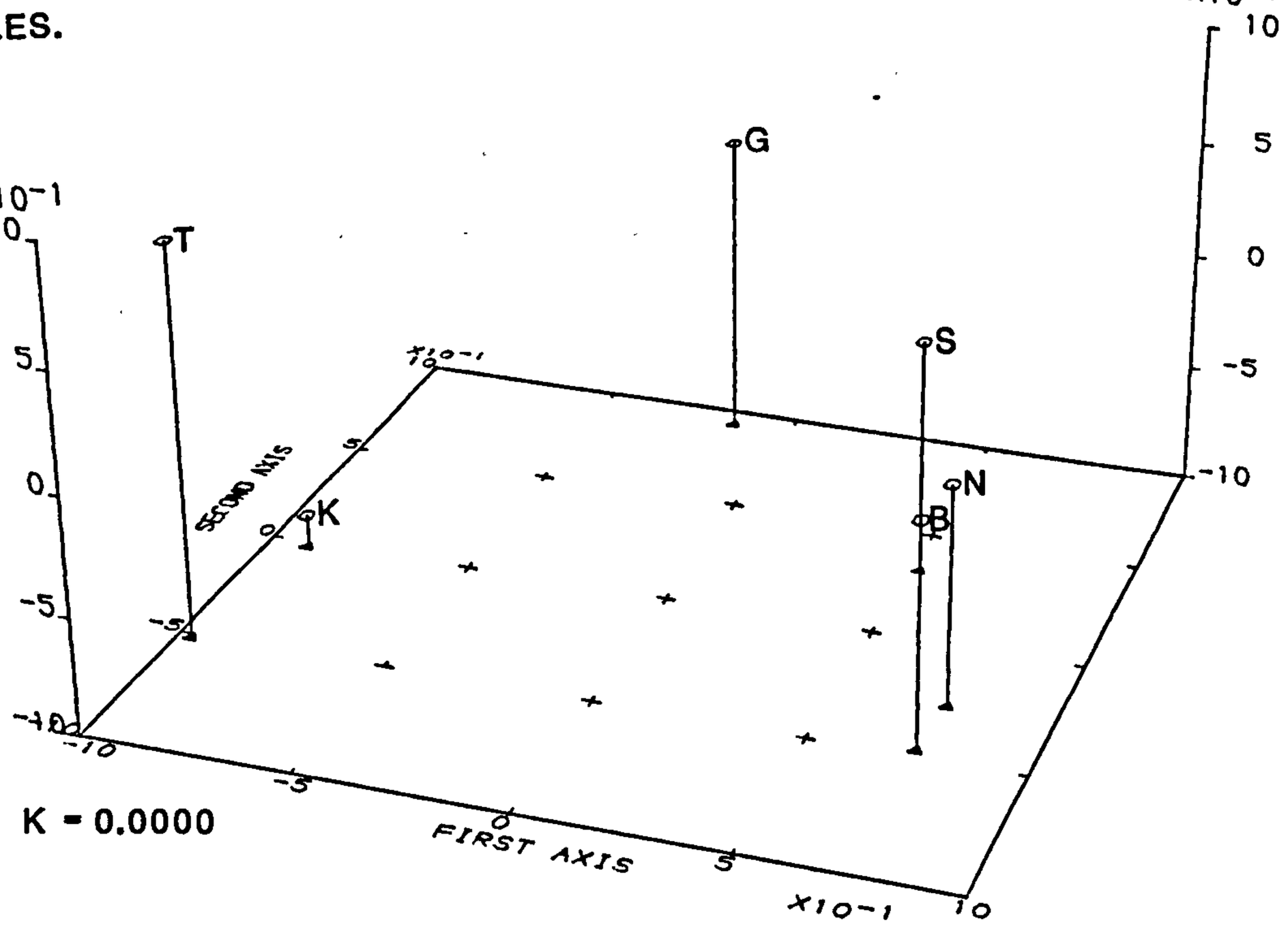
K = 0.0000

Fig. 5.9 Minissa plots in 3 dimensions of 6 African groups.

Distances derived from 60 non-metric traits.

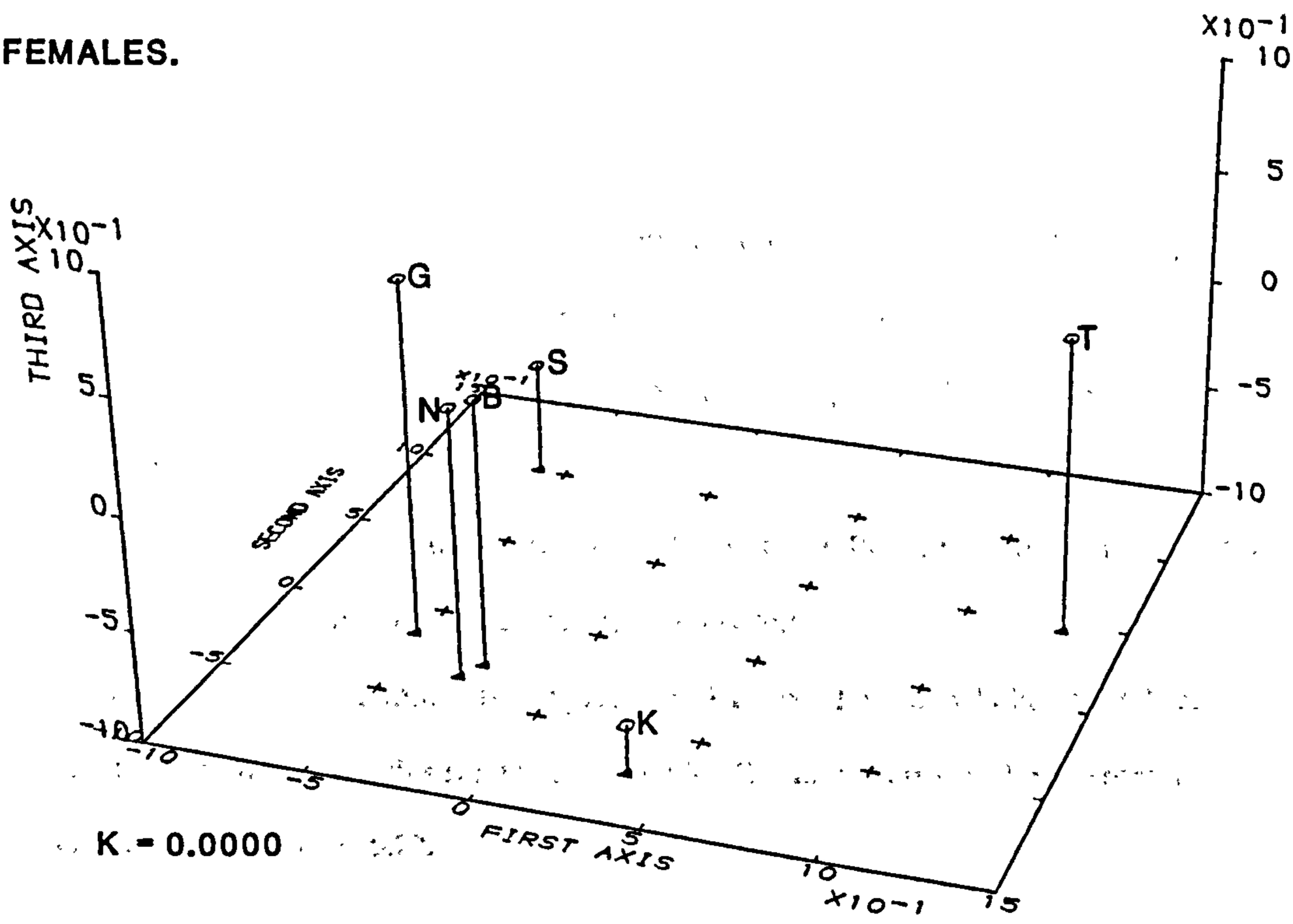
RIGHT SIDE.

MALES.



K = 0.0000

FEMALES.



K = 0.0000

5.3. A comparison of morphological distances for 13 Greek and African groups.

The methods used in section 5.2 to derive and compare distances for 6 African groups are repeated with all 13 groups. As stated at the beginning of this chapter, the aims of this are:

1. to see if the results found in 5.2 are reproduced.
2. to see if pooling the sexes in metric studies can be justified empirically.
3. to examine the plots of the points, in conjunction with those from the 6-group plots (figs 5.1 to 5.9) to see if any conclusions regarding historic relationships of peoples can be drawn.

5.3.1 Generating the morphological distances

Metric distances

Mahalanobis' distances are derived using 9 variables for males only, and then for pooled sexes. These distance matrices are shown in tables 5.17 and 5.18

Non-metric distances

For this analysis, sexes are pooled, following the standard practice in non-metric studies. Two batteries of traits were used, a 32 and a 58 trait battery. The 32 trait set was similar to the 34 trait set, with the following additions and omissions.

a) Posterior ethmoid foramen could not be scored in any of the fragmentary crania from Pyrgos. Also the method of scoring 'jugular foramen bridge' changed between the examination of the Greek and African crania. These two traits were excluded.

b) Palatal and maxillary tori, absent from African groups but observed in the Greek samples, are now included.

c) The four remaining sex-linked traits (12. FHusch, 19. BrCanHy, 30. FlOrbAc and 48. TubPhar) are excluded, since sexes are now pooled.

The 58 trait set is a full set, minus those given in a) above. Freeman-Tukey MMDs are derived for left and right sides separately. The MMDs and their standard errors are presented in tables 5.19 to 5.22.

TABLE 5.17.

MAHALANOBIS DISTANCES (D) FOR 13 GREEK AND AFRICAN POPULATIONS

MALES ONLY.

Pieria	2.454											
Lerna	2.706	1.786										
Athens-M	2.283	2.847	2.417									
Athens-G	2.490	1.137	1.560	2.346								
Fortetsa	3.016	2.676	2.608	3.363	2.713							
Pyrgos	2.880	3.443	2.926	1.174	2.718	4.045						
Giza	1.619	2.018	1.648	1.649	1.652	2.425	2.092					
Kerma	2.274	3.142	2.596	2.852	2.825	2.890	2.969	1.692				
Naqada	2.617	3.350	2.672	2.611	3.002	3.168	2.712	1.732	0.961			
Sedment	1.388	2.779	2.635	2.606	2.613	3.326	2.831	1.451	1.616	1.862		
Badari	3.255	3.865	3.145	3.217	3.487	3.756	3.071	2.359	1.331	0.835	2.309	
Teita	4.168	4.167	3.610	4.406	3.765	2.763	4.513	3.292	2.386	2.710	3.707	2.790
	Sindos	Pieria	Lerna	Athens-M	Athens-G	Fortetsa	Pyrgos	Giza	Kerma	Naqada	Sedment	Badari

9 variables used: **GOL, BNL, XCB, ZYB, NPH, NLH, OBH, NLB, ZMB.**

These values are plotted in fig. 5.10, in which the groups are indentified by the following codes:

Sindos - SI
Pieria - PI
Lerna - LE
Athens-M - AM
Athens-G - AG
Fortetsa - FT
Pyrgos - MP
Giza - GZ
Kerma - KR
Naqada - NQ
Sedment - SD
Badari - BD
Teita - TE

TABLE 5.18.

MAHALANOBIS DISTANCES (D) FOR 13 GREEK AND AFRICAN POPULATIONS

POOLED SEXES.

Pieria	2.153											
Lerna	2.349	1.698										
Athens-M	2.309	2.627	1.962									
Athens-G	2.349	1.446	1.296	1.666								
Fortetsa	2.411	2.038	2.112	2.616	1.976							
Pyrgos	2.623	3.349	2.719	1.098	2.582	3.362						
Giza	1.530	1.913	1.557	1.582	1.714	1.650	2.152					
Kerma	2.683	3.157	2.566	2.741	2.886	2.603	3.129	1.842				
Naqada	2.806	3.250	2.658	2.546	2.932	2.834	2.843	1.839	0.875			
Sedment	1.553	2.676	2.497	2.596	2.779	2.728	2.809	1.470	1.641	1.801		
Badari	3.182	3.474	2.688	2.734	3.087	3.127	3.002	2.130	0.914	0.784	2.026	
Teita	4.669	4.255	3.762	4.384	3.960	2.959	5.061	3.561	2.705	3.062	4.021	2.989
	Sindos	Pieria	Lerna	Athens-M	Athens-G	Fortetsa	Pyrgos	Giza	Kerma	Naqada	Sedment	Badari

9 variables used: **GOL, BNL, XCB, ZYB, NPH, NLH, OBH, NLB, ZMB.**

These values are plotted in fig. 5.11, in which the groups are indentified by the following codes:

Sindos -	SI
Pieria -	PI
Lerna -	LE
Athens-M -	AM
Athens-G -	AG
Fortetsa -	FT
Pyrgos -	MP
Giza -	GZ
Kerma -	KR
Naqada -	NQ
Sedment -	SD
Badari -	BD
Teita -	TE

TABLE 5.19.

MMD FOR 13 GREEK AND AFRICAN POPULATIONS (POOLED SEXES)

LEFT side only used for bilateral traits.

32 traits used: 2, 4-7, 9-10, 14, 16-18, 20, 21, 23-26, 31, 36, 39-41, 44, 46, 50, 52-57, 60.

Upper figure - Freeman-Tukey MMD
Lower figure - St. error of MMD
* - MMD significant. ($p < 0.05$)

	Sindos	Pieria	Lerna	Athens-M	Athens-G	Fortetsa	Pyrgos	Giza	Kerma	Naqada	Sedment	Badari
Pieria	-0.019 0.023											
Lerna	-0.005 0.025	-0.011 0.025										
Athens-M	-0.004 0.025	0.010 0.025	0.005 0.027									
Athens-G	-0.015 0.029	-0.016 0.030	0.016 0.032	-0.046 0.031								
Fortetsa	-0.026 0.050	-0.044 0.051	0.007 0.054	0.019 0.053	-0.120 0.057							
Pyrgos	0.004 0.037	0.033 0.037	-0.009 0.039	0.054 0.039	0.060 0.043	0.042 0.065						
Giza	0.072* 0.014	0.058* 0.014	0.039* 0.016	0.014 0.016	0.020 0.020	0.033 0.042	0.067* 0.028					
Kerma	0.069* 0.014	0.054* 0.015	0.038* 0.017	0.001 0.017	0.042* 0.021	0.106* 0.043	0.040 0.029	0.024* 0.006				
Naqada	0.085* 0.014	0.050* 0.015	0.042 0.016	0.024 0.016	0.020 0.021	0.040 0.042	0.047 0.028	-0.003 0.005	0.011 0.006			
Sedment	0.063* 0.015	0.041* 0.016	0.025 0.018	-0.001 0.017	0.031 0.022	0.081 0.043	0.045 0.030	0.010 0.006	0.005 0.007	0.006 0.007		
Badari	0.085* 0.016	0.059* 0.017	0.015 0.019	0.023 0.018	0.040 0.023	0.065 0.044	0.016 0.031	0.009 0.007	0.020* 0.008	0.005 0.008	-0.004 0.009	
Teita	0.085* 0.015	0.070* 0.015	0.064* 0.017	0.036* 0.017	0.037 0.021	0.078 0.043	0.043 0.029	0.013* 0.006	0.006 0.007	0.007 0.006	0.014* 0.007	0.014 0.008

These values are plotted in fig. 5.12, in which the groups are indentified by the following codes:

Sindos -	SI
Pieria -	PI
Lerna -	LE
Athens-M -	AM
Athens-G -	AG
Fortetsa -	FT
Pyrgos -	MP
Giza -	GZ
Kerma -	KR
Naqada -	NQ
Sedment -	SD
Badari -	BD
Teita -	TE

TABLE 5.20.

MMD FOR 13 GREEK AND AFRICAN POPULATIONS (POOLED SEXES)

RIGHT side only used for bilateral traits.

32 traits used: 2, 4-7, 9-10, 14, 16-18, 20, 21, 23-26, 31, 36, 39-41, 44, 46, 50, 52-57, 60.

Upper figure - Freeman-Tukey MMD
Lower figure - St. error of MMD.
* - MMD significant. ($p < 0.05$)

	Sindos	Pieria	Lerna	Athens-M	Athens-G	Fortetsa	Pyrgos	Giza	Kerma	Naqada	Sedment	Badari
Pieria	-0.015 0.023											
Lerna	-0.027 0.027	0.016 0.028										
Athens-M	0.014 0.024	0.040 0.025	-0.017 0.029									
Athens-G	-0.030 0.029	-0.039 0.030	-0.004 0.034	-0.027 0.031								
Fortetsa	-0.047 0.043	0.009 0.045	-0.039 0.048	-0.047 0.045	-0.067 0.050							
Pyrgos	-0.074 0.048	-0.047 0.049	-0.075 0.053	-0.033 0.051	-0.052 0.054	-0.091 0.069						
Giza	0.075* 0.014	0.068* 0.015	0.020 0.019	0.025 0.015	0.021 0.021	-0.026 0.035	0.008 0.041					
Kerma	0.062* 0.014	0.056* 0.015	0.027 0.019	0.029 0.016	0.021 0.021	-0.024 0.035	-0.008 0.041	0.014* 0.006				
Naqada	0.073* 0.014	0.056* 0.015	0.016 0.019	0.019 0.016	0.013 0.021	0.000 0.035	-0.004 0.041	-0.002 0.005	0.020* 0.006			
Sedment	0.064* 0.015	0.044* 0.016	0.035 0.020	0.027 0.017	-0.014 0.022	-0.022 0.036	0.010 0.042	0.012* 0.006	0.041* 0.007	0.001 0.007		
Badari	0.073* 0.016	0.043* 0.017	0.014 0.021	0.021 0.018	-0.004 0.023	-0.011 0.037	0.008 0.043	0.008 0.008	0.036* 0.008	-0.003 0.008	-0.005 0.009	
Teita	0.105* 0.015	0.057* 0.016	0.055* 0.020	0.050* 0.016	0.029 0.021	0.025 0.036	0.032 0.041	0.019* 0.006	0.020* 0.007	0.005 0.006	0.015* 0.007	0.004 0.008

These values are plotted in fig. 5.13, in which the groups are indentified by the following codes:

Sindos -	SI
Pieria -	PI
Lerna -	LE
Athens-M -	AM
Athens-G -	AG
Fortetsa -	FT
Pyrgos -	MP
Giza -	GZ
Kerma -	KR
Naqada -	NQ
Sedment -	SD
Badari -	BD
Teita -	TE

TABLE 5.21.

MMD FOR 13 GREEK AND AFRICAN POPULATIONS (POOLED SEXES)

LEFT side only used for bilateral traits.

58 traits used (all except 29, 47)

Upper figure - Freeman-Tukey MMD
Lower figure - St. error of MMD
* - MMD significant. ($p < 0.05$)

	Sindos	Pieria	Lerna	Athens-M	Athens-G	Fortetsa	Pyrgos	Giza	Kerma	Naqada	Sedment	Badari
Pieria	-0.022 0.018											
Lerna	-0.013 0.019	-0.011 0.019										
Athens-M	-0.006 0.019	0.023 0.019	-0.011 0.021									
Athens-G	0.005 0.024	0.028 0.024	0.047 0.025	-0.027 0.026								
Fortetsa	-0.024 0.039	0.010 0.039	0.041 0.041	-0.002 0.041	-0.092 0.045							
Pyrgos	0.019 0.034	0.050 0.035	0.019 0.036	0.032 0.037	0.120* 0.041	0.036 0.055						
Giza	0.085* 0.010	0.100* 0.011	0.053* 0.012	0.026* 0.012	0.058* 0.017	0.024 0.033	0.086* 0.028					
Kerma	0.078* 0.011	0.085* 0.011	0.059* 0.012	0.021 0.013	0.060* 0.017	0.077* 0.033	0.082* 0.029	0.024* 0.004				
Naqada	0.105* 0.011	0.110* 0.011	0.083* 0.012	0.046* 0.012	0.053* 0.017	0.029 0.033	0.070* 0.028	0.004 0.004	0.020* 0.004			
Sedment	0.072* 0.012	0.073* 0.012	0.042* 0.013	0.016 0.013	0.048* 0.018	0.059 0.034	0.085* 0.029	0.013* 0.004	0.015* 0.005	0.017* 0.005		
Badari	0.086* 0.012	0.096* 0.013	0.044* 0.014	0.028* 0.014	0.049* 0.019	0.035 0.034	0.065* 0.030	0.003 0.006	0.014* 0.006	0.001 0.006	-0.009 0.007	
Teita	0.088* 0.011	0.117* 0.011	0.078* 0.013	0.049* 0.013	0.047* 0.018	0.067* 0.033	0.114* 0.029	0.040* 0.004	0.022* 0.005	0.042* 0.004	0.046* 0.005	0.028* 0.006

These values are plotted in fig. 5.14, in which the groups are indentified by the following codes:

Sindos -	SI
Pieria -	PI
Lerna -	LE
Athens-M -	AM
Athens-G -	AG
Fortetsa -	FT
Pyrgos -	MP
Giza -	GZ
Kerma -	KR
Naqada -	NQ
Sedment -	SD
Badari -	BD
Teita -	TE

TABLE 5.22.

MMD FOR 13 GREEK AND AFRICAN POPULATIONS (POOLED SEXES)

RIGHT side only used for bilateral traits.

58 traits used (all except 29, 47)

Upper figure - Freeman-Tukey MMD
Lower figure - St. error of MMD.
* - MMD significant. ($p < 0.05$)

	Sindos	Pieria	Lerna	Athens-M	Athens-G	Fortetsa	Pyrgos	Giza	Kerma	Naqada	Sedment	Badari
Pieria	0.018 0.018											
Lerna	-0.007 0.021	0.006 0.021										
Athens-M	0.019 0.019	0.011 0.020	-0.026 0.023									
Athens-G	-0.029 0.023	-0.028 0.023	-0.031 0.027	-0.040 0.025								
Fortetsa	-0.058 0.033	0.031 0.034	-0.025 0.037	-0.041 0.035	-0.069 0.039							
Pyrgos	-0.032 0.038	-0.040 0.039	-0.056 0.042	-0.060 0.041	-0.056 0.043	-0.069 0.055						
Giza	0.092* 0.010	0.107* 0.011	0.030* 0.014	0.034* 0.012	0.043* 0.016	0.015 0.027	0.035 0.032					
Kerma	0.061* 0.011	0.098* 0.011	0.037* 0.015	0.031* 0.013	0.036* 0.017	-0.027 0.027	0.020 0.033	0.025 0.004				
Naqada	0.092* 0.010	0.114* 0.011	0.050* 0.014	0.036* 0.012	0.050* 0.016	0.0130 0.027	0.033 0.033	0.004 0.004	0.028* 0.004			
Sedment	0.081* 0.011	0.099* 0.012	0.054* 0.015	0.037* 0.013	0.024 0.017	0.012 0.028	0.041 0.033	0.020* 0.005	0.040* 0.005	0.002 0.005		
Badari	0.074* 0.012	0.110* 0.013	0.048* 0.016	0.048* 0.014	0.032 0.018	0.008 0.029	0.061 0.034	0.015* 0.006	0.037* 0.006	-0.003 0.006	0.003 0.007	
Teita	0.099* 0.011	0.101* 0.012	0.059* 0.015	0.049* 0.013	0.042* 0.017	0.036 0.027	0.079* 0.033	0.049* 0.004	0.030* 0.005	0.044* 0.004	0.061* 0.005	0.037* 0.006

These values are plotted in fig. 5.15, in which the groups are indentified by the following codes:

Sindos -	SI
Pieria -	PI
Lerna -	LE
Athens-M -	AM
Athens-G -	AG
Fortetsa -	FT
Pyrgos -	MP
Giza -	GZ
Kerma -	KR
Naqada -	NQ
Sedment -	SD
Badari -	BD
Teita -	TE

5.3.2. Multidimensional scaling

As with the 6 group analysis, MINISSA was used. Since there are 13 groups, up to 10 dimensions may be needed to produce a plot with acceptable stress values (as shown by the coefficient of alienation, K). The metric matrices produced acceptable (see figs 5.10 and 5.11) plots in 3 dimensions: though a higher number of dimensions will give a smaller K, the advantage of visual inspection of the points will have been lost. The same argument is used for non-metric traits (plots shown in figs 5.12-5.15), whose value of K is greater, but still judged acceptable. However, the coordinates in 7 dimensions were also recorded for later use.

5.3.3. Procrustes analysis.

Table 5.23 shows the results of comparing the distance matrices for:

1. Metric variates: male vs. pooled sexes
2. Non-metric traits: left vs. right side (for 3-D and 7-D plots)
3. Metric variates vs. non-metric traits.

The rationale behind this choice of tests is to demonstrate whether pooling of the sexes affects the Mahalanobis' distance, whether the information contained in left and right sides of the skull is equivalent, and whether both types of trait carry equivalent information on group relationships.

5.3.4. Summary

The two metric plots (figs. 5.10 and 5.11) are highly congruent, as shown by visual appraisal and the results of the Procrustes analysis ($R^2 = 0.045$). This provides evidence that the pooling of sexes in metric studies may be justified if sample sizes are otherwise inadequate. It could be countered that, if pooling the sexes makes so little difference, then why bother to pool in the first place? The answer to this is that confidence in the meaningfulness of the results is dependent on adequate sample size. This is illustrated by tables A1.3-A1.8 in appendix 1. These show the F-values for the significance of D^2 derived (using 'CVAID) for males only, and pooled sexes, for 11 and 5 group sets. In both analyses,

the pooled-sex tables show marginally more D^2s which are significantly different from zero. In practice, the significance of the D^2 (as given by the F-test) depends more on the sample size than the size of D^2 itself.

With regard to left-right correspondence, the results of section 5.2 are confirmed; even poorer correspondence is found for the 13 groups (R^2 = 0.572, 0.435 for 32 and 58 traits respectively). Better agreement is obtained when a higher number of dimensions is considered, but the R^2 values are still of the same order as those obtained in the 6 group analysis. It seems that the information contained in right and left sides of the skull is different; alternatively, the sample sizes employed here (even in the 6 group analysis) are inadequate for the statistical assumptions underlying the MMD formula (Sjøvold 1973) to be valid.

Metric (pooled sex) and non-metric comparisons reiterate the findings of the 6 group comparison, that different information is contained in the two types of trait. Having established this, the question of which type of information is more useful may legitimately be asked. The results of this study indicate that metric distances are more useful as indicators of genetic distance since:

a) The pattern of population relationships is similar in both male and female crania, and

b) This same pattern is generally retained through different sets of traits.

It is claimed that non-metric traits make better use of the information in poorly preserved and deformed specimens, and also in small samples since separation of the sexes is unnecessary. The results of this study rebut this claim, demonstrating that:

a) Metric studies can utilise incomplete (though not deformed) crania, provided that the combined groups contain a sufficient number of whole specimens. This is done by calculating the Mahalanobis' distance using the means from all possible measurements.

b) For metric traits, the sexes can be pooled to improve sample size, without disturbing the pattern of relationship shown when one sex is used, or notably violating the method's statistical assumptions.

TABLE 5.23

COMPARISON OF PAIRS OF DISTANCE MATRICES

FOR 13 GREEK AND AFRICAN GROUPS

(USING PROCRUSTES ANALYSIS).

Pairs compared	R2 (residual variance)
METRIC (3-D plots)	
9 variates	
Males vs. Pooled	0.045
NON-METRIC	
Left side vs. Right side	
32 traits (3-D plots)	0.572
32 traits (7-D plots)	0.400
58 traits (3-D plots)	0.436
58 traits (7-D plots)	0.331
METRIC vs. NON-METRIC (Metric based on 9 variates)	
Pooled vs. different trait sets	
32 traits - left side	0.688
32 traits - right side	0.637
58 traits - left side	0.533
58 traits - right side	0.464

Fig. 5.10

Minissa plot

In 3 dimensions

of 13 groups from

Greece and Africa.

Distances derived

.

rom 9 metric traits.

MALES ONLY.

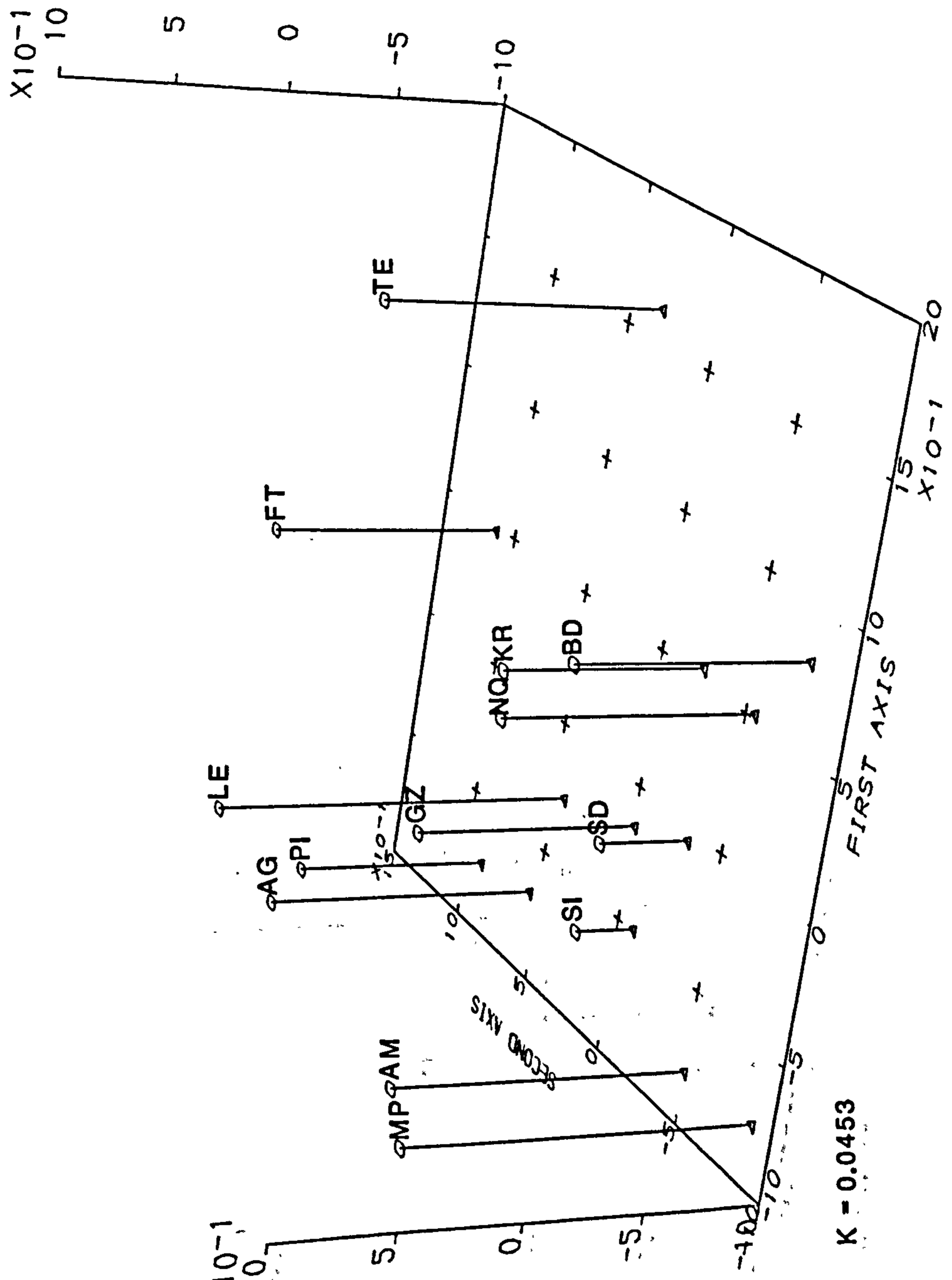


Fig. 5.11

Minissa plot

In 3 dimensions

of 13 groups from

Greece and Africa.

Distances derived

from 9 metric traits.

SEXES POOLED.

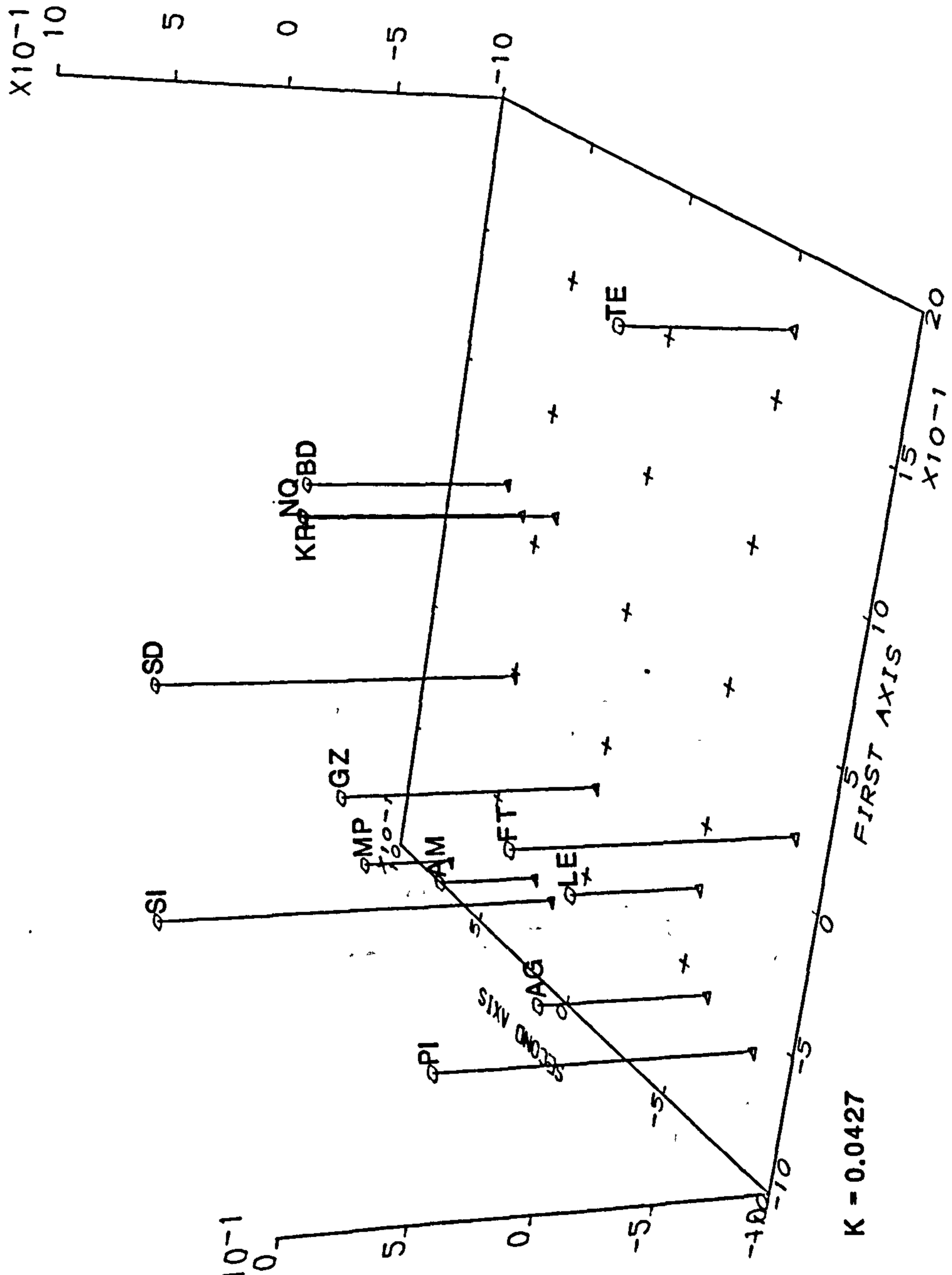
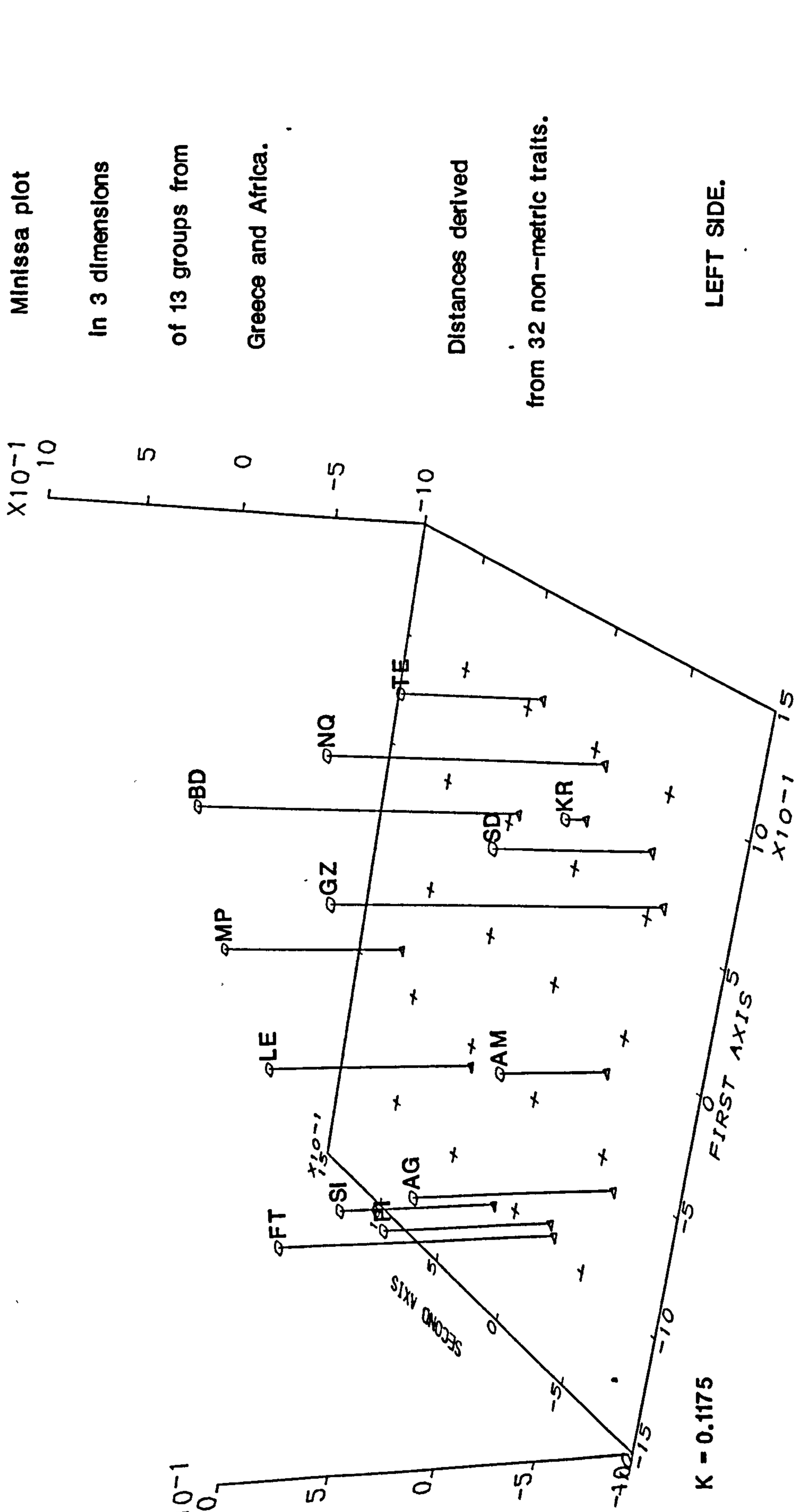


Fig. 5.12 Minissa plot in 3 dimensions from Distances derived of 13 groups from 32 non-metric traits. Greece and Africa.



LEFT SIDE.

Fig. 5.13

Minissa plot

In 3 dimensions

of 13 groups from

Greece and Africa.

Distances derived

32 non-metric traits.

RIGHT SIDE.

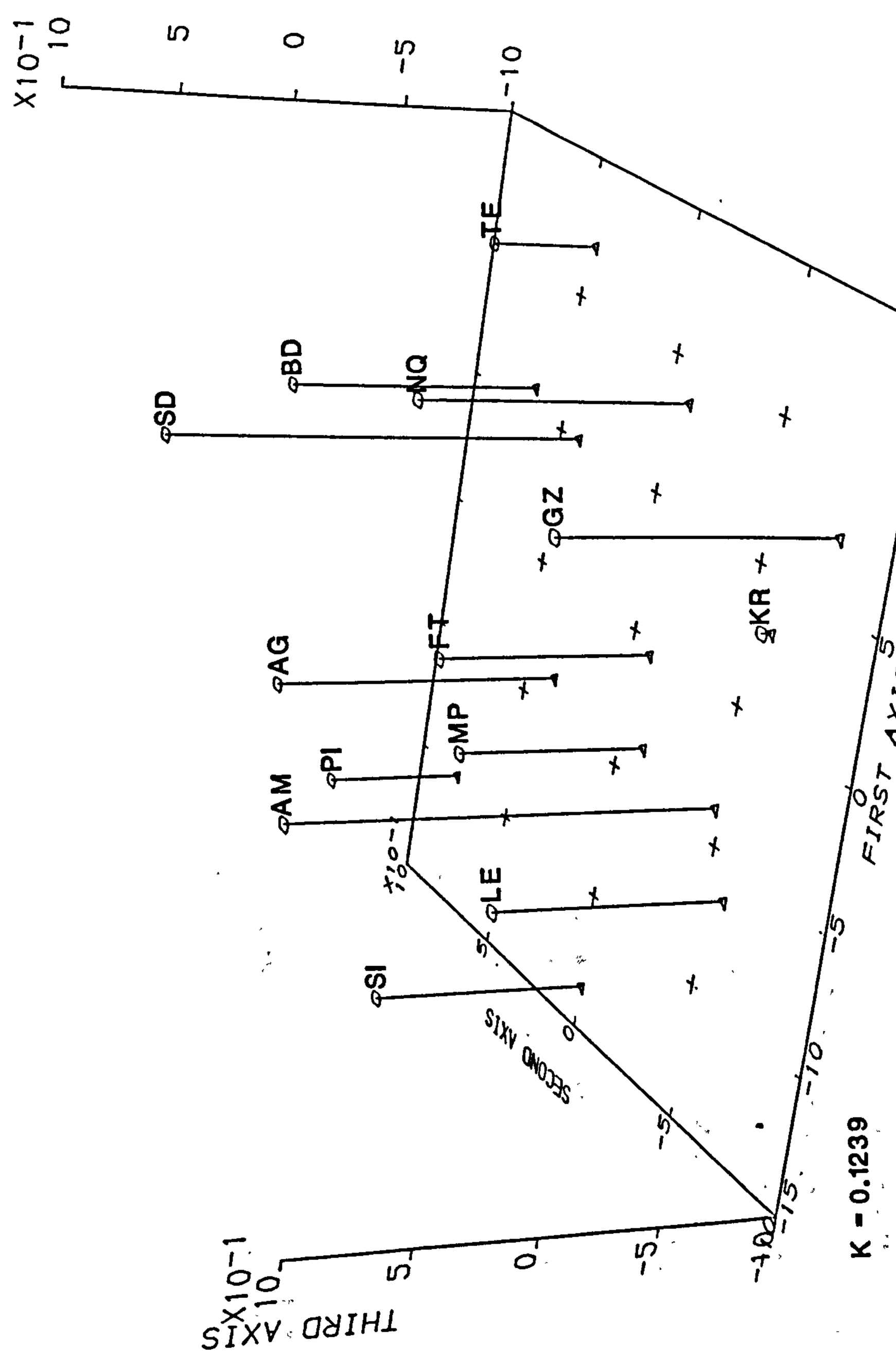


Fig. 5.14

Minissa plot

In 3 dimensions

of 13 groups from

Greece and Africa.

Distances derived

from 58 non-metric traits.

LEFT SIDE.

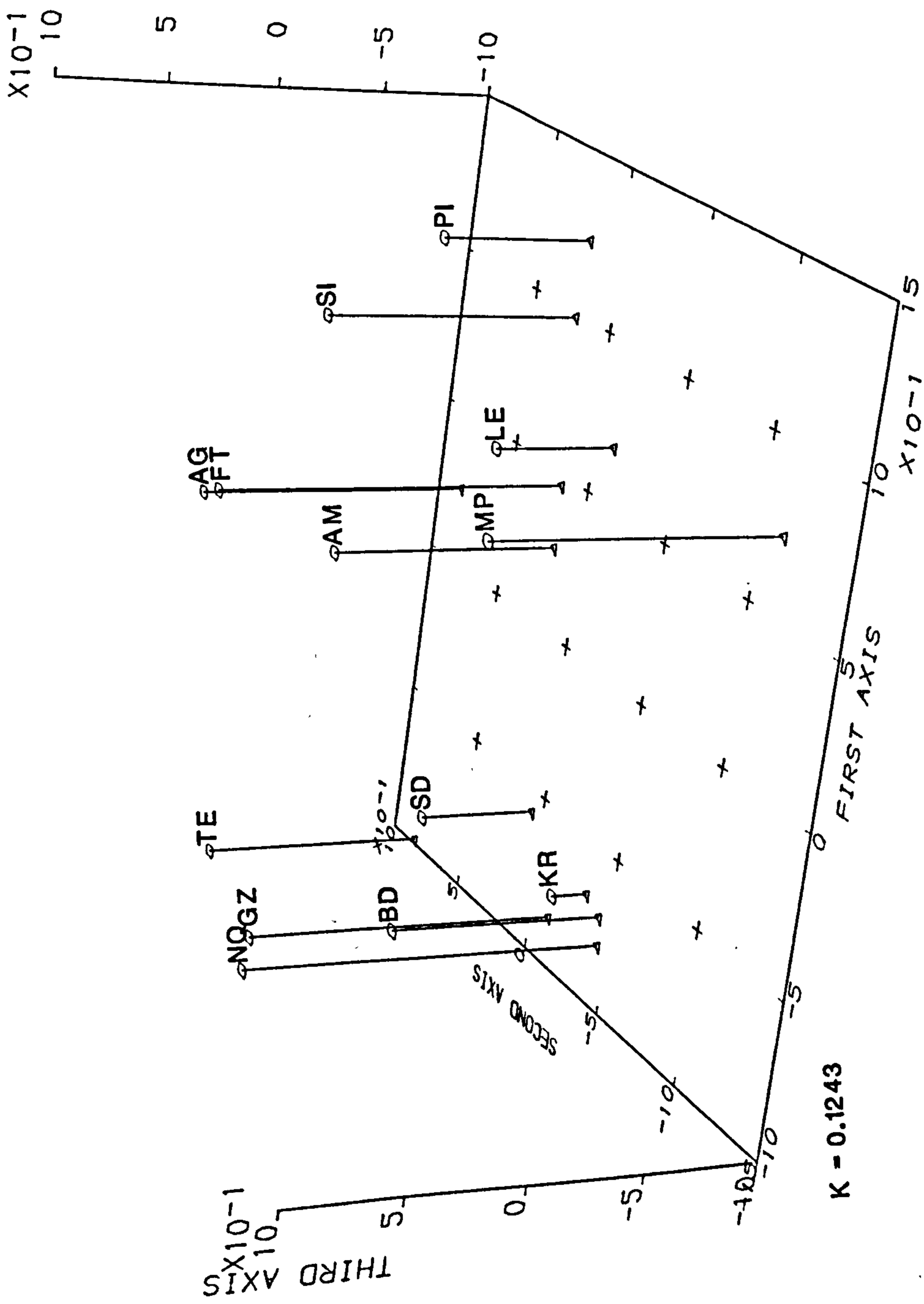
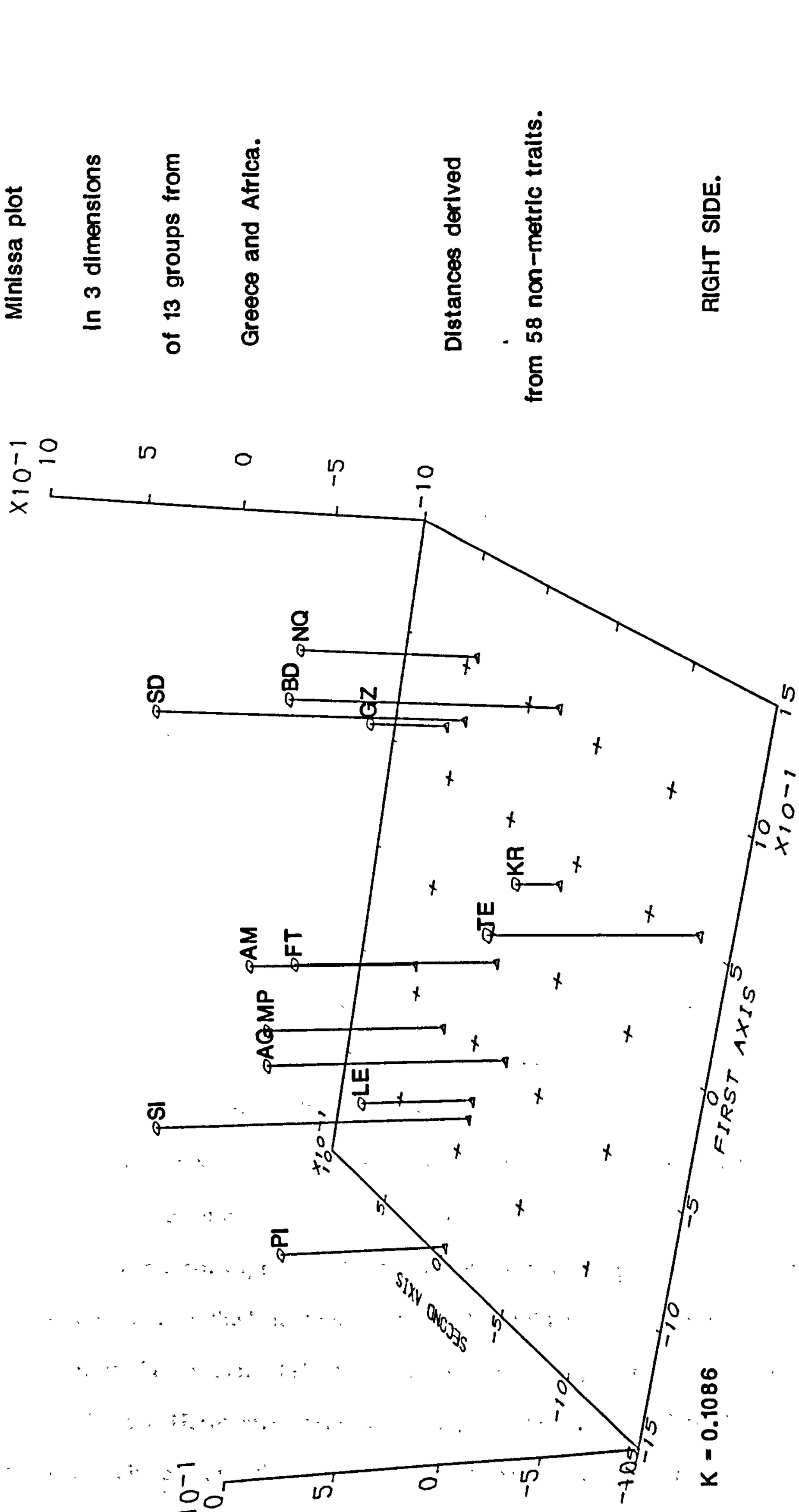


Fig. 5.15 Minissa plot of 13 groups from Greece and Africa. In 3 dimensions from 58 non-metric traits. Distances derived



Population relationships of the Ancient Greeks and Egyptians.

Metric plots (figs. 5.10 and 5.11).

Examination of the metric plots reveals the following general pattern of relationships. The Teita crania, as expected, are distinct from all others. Predynastic Naqada and Badari form a separate cluster with 12-15th Dynasty Kerma. These results are consistent with those shown by the 6 group analysis. The Egyptian and Greek sites are in general separate, though Giza and Sedment seem to show some affinity with the Greeks, especially those from Lerna. Historical and archaeological evidence (Petrie 1907) suggests that between 600 and 300 B.C., Giza contained a considerable number of Greek immigrants. Angel (1971) similarly commented on the cosmopolitan characteristics of the archaeological and human remains from Middle Helladic Lerna. The position of 9th Dynasty Sedment is more difficult to explain, but other workers (e.g. Woo 1930, and more recently, Keita 1983) have commented on this site's distinctiveness from other Egyptian series. Fortetsa seems to be distinct both from Greeks and Egyptians; this does not necessarily indicate that these Early Christians were immigrants. The small sample size, or possible close family relationship of the inhabitants of this ossuary could account for the group's apparent distinctiveness.

Conclusions regarding individual Greek sites must be more tentative since the sample sizes are so small. However, Musgrave and Evans' (1980) conclusion that the Minoans did not come from Egypt seems to be borne out. The proximity of Middle Minoan Pyrgos to Mycenaean Athens is interesting in the light of the cultural similarity of the Minoans and Mycenaeans (Chadwick 1976, Warren 1975). The Athenean crania derive mainly from Mycenaean chamber tombs under the Agora. Surprisingly, Lerna, which also shows much evidence of the Mycenaean culture, is separate from them.

Amongst the Greeks, Sindos appears to be the most distinctive group; though whether this suggests a Balkan origin for the Macedonian people is beyond the scope of this study. The isolated settlement of Pieria is most similar to the roughly contemporary population of Geometric-Archaic Athens. However, any conclusions regarding the affinity of the Greek people must be extremely tentative, since earlier investigative plots (not included in this

work) from the 'CVAID' program, which show individual crania as well as group means, revealed much overlap of the groups. The fact that few of the F-values of the D^2 reach significance (see tables A1.3-A1.8 in appendix 1) similarly attests the overall homogeneity of the Greek race.

Non-metric plots (figs. 5.12-15)

The non-metric plots reveal a more confused picture of the pattern of relationships. Again the Greek and Egyptian sites are separated, the clustering being more distinct when 58 traits are considered. The distinctiveness of the Teita varies in each plot, being most separated in the 58 trait-right sided plot. The same plot puts Kerma intermediate between the Teita and the rest of the Egyptian sites; others cluster Kerma amongst the Egyptians. No clear pattern is apparent amongst the Greeks, but there is a possible separation of Sindos and Pieria (both northern sites) from the rest of the Greek sites. Myrtos Pyrgos, where it is not distinct from all other sites, shows affinities with the Greeks rather than the Egyptians, as in the metric plots. The closeness to Greek sites of Giza and Sedment is not seen here.

An examination of the tables of divergences, with their standard errors, reveals little that is not apparent in the plots, but with more scope for confusion. For the 32-trait analysis, no significant distances are seen amongst the Greek sites. In fact, out of the 21 distances, 11 are negative, indicating no difference between the groups. However, for the left-side MMDs, Pyrgos has positive values for all sites except Lerna; the right-side MMDs for Pyrgos are negative in all cases. A similar anomaly is seen in the 58-trait analysis, where Pyrgos appears more distinct (the Geometric-Athens MMD is significant) on the left side, but indistinguishable from other Greek groups (all 6 values are negative) on the right.

Comparing the Greeks and Africans, the northern Greek sites (Sindos and Pieria) are distinct (i.e. have significant MMDs) from all African Groups in all 4 analyses. The separation of the other Greek and African sites varies in each analysis, though the (more reliable?) 58-trait set separates Lerna and the Athenian sites from the Africans. Fortetsa is less distinct, while Pyrgos is distinct for the left-sided traits but the MMDs fail (with the exception of the Teita) to reach significance on the right.

RESULTS

Amongst the Africans, the Teita are distinct from the Egyptians in both 58-trait analyses, but only from Giza and Sedment in both the 32-trait sets. Kerma is distinct from all other groups in both 58-trait sets and the right-sided 32-trait set. In all 4 analyses the similarity of Badari and Naqada is seen, and also of Giza and Naqada, and Sedment and Badari. Sedment is usually distinct from Giza, in contrast to the metric picture.

6

INTERPRETATION OF RESULTS AND DISCUSSION.

This study was undertaken in response to the long-standing disagreement between anthropologists regarding the relative merits of metric and non-metric traits in palaeogenetics (Berry 1979, Musgrave and Evans 1980). Its aim was to demonstrate once-and-for-all whether non-metric or metric traits are more deserving of study when population affinities are to be investigated. This is not the first time such a study has been undertaken. Previous studies, however, (Rightmire 1972, Zegura 1975, Ossenberg 1977) have not led to a consensus of opinion. This final chapter is concerned with assessing the impact of the present work on the metrics vs. non-metrics controversy.

6.1. Summary and discussion of the main findings.

The three main findings of this study will now be discussed:

1. *Metric distances derived from both male and female crania reveal a congruent pattern of taxonomic relationships. This is not the case with non-metric distances.*

The congruence of the matrices of male and female metric distances confirms the findings of other workers. Zegura (1975) and Ossenberg (1977) each reported a Spearman's rank-order correlation (*rho*) of 0.92 between the sexes in 12 Eskimo groups and 5 Alaskan populations respectively. Spearman's coefficients calculated from Laughlin and Jørgensen's (1956) results show a fairly good correspondence (*rho*=0.77) between the sexes. Howells (1973) also noted a "very detailed correspondence in results for the two sexes obtained separately" in his study of 17 world-wide populations.

The poor congruence between the sexes for non-metric distances confirms the findings of Zegura (*rho* = 0.41) and of Laughlin and Jørgensen (*rho* =0.04). Ossenberg (1976), conversely, found high male-female correlation for the MMDs in each of 3

North American groups (*rho* values of 0.88, 0.94 and 0.96). However, Ossenberg's coefficients are not in this case produced by comparing the elements of male and female distance matrices. She calculates MMD values for males and females from one group in relation to 15 other pooled-sex groups. It is arguable whether the results of this method (equivalent to testing 1 row of a distance matrix) are commensurable with those used by Zegura, where the whole matrix is tested. Since the elements of a distance matrix may be interdependent (most likely for D^2 values, which are constrained to be Euclidian) Ossenberg's method may be preferred to Zegura's. [1] However, it could be argued that the complex pattern of interactions portrayed in a complete distance matrix provides a more sensitive test.

It is difficult to account for the poor congruence of the sexes in non-metric distances. Although the practice of exogamy immediately springs to mind as an explanation, further thought must cause it to be rejected since:

1) there is no evidence of widespread exogamy amongst the ancient Egyptians. Though the Teita are known to be exogamous, Howells (1973), like Kitson (1931), found no evidence of increased variability in the female crania.

2) the long term practice of exogamy would not maintain different gene-pools in the sexes, since the progeny of exogamous unions would have similarities to both parents, such that tribes which interact in this way would tend to become genetically homogeneous.

3) if exogamy were responsible, these differences would be expected to show up in the metric, as well as the non-metric distances.

This sex difference is difficult to explain unless the hypothesis that human non-metric traits are predominantly under genetic control is rejected. Although there is evidence for the genetic basic of these traits in laboratory animals, these populations cannot reflect the genetic and environmental circumstances found in nature, and

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[1] Note that this problem of interdependence does not arise with Procrustes analysis.

caution must be exercised if these results are to be applied elsewhere (Richtsmeier and McGrath 1986).

2. *Metric distances derived from different numbers of traits show fairly good congruence. Non-metric distances derived from different trait sets are more variable but show, in general, a poorer correspondence. Similarly, there is very little agreement between metric and non-metric distances.*

These results must be interpreted in the light of the non-specificity hypothesis (Sokal and Sneath 1963), which implies that infra-specific taxonomies based on different sets of skeletal attributes should be equivalent. In all cases in the present work, metric and non-metric distances show poor agreement. Laughlin and Jørgensen's (1956) work and Rightmire's (1972) study produced similar results; Zegura (1975) also noted that the non-specificity hypothesis was untenable. Ossenberg (1977), however, demonstrated a reasonable concurrence between male and female (*rho* = 0.77, 0.84 respectively) metric and pooled non-metric distance matrices. Corruccini (1974) also found good correlation (r=0.78) among subdivisions of U.S. Black and White crania. When comparing these studies, it should be remembered that the number of groups, number of traits and distance statistics used differs in each of them.

Although metric and non-metric traits seem to hold different information, within each type there is rather more agreement. Analyses based on different sets of cranial measurements generally concur. This effect has similarly been shown by Musgrave and Evans (1980) and Keita (1983). While this could be due to the fact that the smaller variable sets are subsets of the larger ones, this argument applies equally well to the non-metric case, in which congruence is generally present to a lesser extent.

It has been noted in this study that the agreement between subsets of non-metric variables is better for females than males, while the opposite is true for metric traits. Although this isolated result requires substantiation, it has interesting implications in the light of the controversial theory, reviewed by Stinson (1985),

that males are less buffered against the effect of environment during growth and development. The strongest support for this theory comes from studies of the pre-natal period, which is a crucial time in the development of many discrete skeletal traits. The greater congruence of the 6 non-metric trait sets in females supports this theory. However, subsidiary evidence, such as that left/right correspondence is greater in females, is not found; over the 3 trait sets the averages for males (R^2=0.265, range 0.91-0.48) and females (R^2=0.261, range 0.20-0.35)) are almost identical, though the male values have a greater range. The greater correspondence of male metric distances does not contradict this theory, because of the importance of post-natal growth on cranial dimensions.

3. *Non-metric distances derived from traits on the left side of the cranium do not correspond as closely as expected with those derived from right-sided traits.*

In most of the analyses, there is only a moderate agreement between the left and right-sided distances. This side difference is more pronounced in the 13 group analysis where the sexes are pooled. The increase is not entirely due to the inclusion of the Greek groups with their smaller sample sizes, since:

a) the pooled sex Greek groups are often as large as the single-sex Egyptian, as can be seen from an inspection of the tables in appendix 2.

b) examination of the plots (figs 5.12-5.15) shows the major disagreement to centre on the positions of Kerma and Sedment in both variable sets.

Previous studies of left/right variation have concluded that side differences are practically irrelevant (Perizonius 1979a, Cosseddu, Floris and Vona 1979). Cosseddu, Floris and Vona, studying Sardinian crania, derived MMDs for the left and right side in males and females separately, and then in pooled sexes. Their MMDs were negative for the separated sexes, but a small (non-significant) positive value was found in the pooled group. This suggests that pooling of the sexes in the 13 group study could have influenced the left/right relationships. This suggestion is

seemingly contradicted by the fact that the 32-trait set, from which sex-linked traits have been removed, shows poorer left-right congruence than the 58-trait set (note however, that the Greek sites were not tested for sex-linked traits).

Within the 6 group analyses, the level of agreement between the sides varies from very good (R^2= 0.09 for 60 trait, male) to moderate (R^2= 0.38 for 34 trait, male). Unlike the results of male/female and metric/non-metric comparisons, it is difficult to describe objectively the left/right correspondence presented here as good or poor. During some of the preliminary analyses (not presented in this work) where other trait batteries were analysed, however, it was consistently found that left/right correspondence was poor. Hence, it is here concluded that, although a moderate left/right correspondence is apparent, rather more agreement would have been expected. This difference in the information contained in the two sides of the skull appears to contradict the theory that fluctuating asymmetry is caused by random 'accidents' during development.

Richtsmeier and McGrath (1986) uncover further evidence that trait expression on the left and right sides may not be equivalent. They compared the results of two previous studies (Cheverud and Buikstra 1981, McGrath et al. 1984), which derived heritability estimates derived for hyperostotic/hypostotic and foraminal traits in the Cayo Santiago macaques. Although both studies used the same sample, they used different sides for scoring the bilateral traits. McGrath et al. found that they could not confirm the pattern of heritabilities on the left side that Cheverud and Buikstra had found on the right.

In summary, this study has shown that the characteristics of distances based on metric traits are consistent with those expected of a genetic or taxonomic distance. The pattern of relationship between the groups, as revealed by the metric plots, is also reasonable in the light of present archaeological knowledge. Non-metric traits, however, produce distances which behave in an erratic manner, and the population relationships suggested by non-metric plots is problematical. Metric variation, therefore, must be regarded as the more

reliable indicator of population affinity. This study is open to the criticism that the metric variables, having been taken by different workers, are subject to inter-worker error. However, the consistency of the metric results, and the discovery that non-metric traits are subject to a considerable degree of intra-worker error, yield the conclusion that the results are nonetheless valid.

6.2. The genetic basis of non-metric traits - revisited.

In chapter 2, the evidence was reviewed which showed that non-metric traits have a strong genetic basis. The disagreement between male and female non-metric distances does not concur with this supposition. Recently, some workers have begun to question this assumption of a strong genetic component. Richtsmeier and McGrath (1986), studying mice, found that in only 4 of 35 traits could they arrive at a significant heritability value. Noting that these results were consistent with those of Self and Leamy (1978) and Searle (1954), they suggest that "historically accepted assumptions about heritability of non-metric traits require continued close scrutiny".

The contention that non-metric traits are not genetic is not easily accepted in the face of counter-evidence from numerous studies in mice (e.g. Grüneberg 1963), macaques (e.g. Cheverud and Buikstra 1981) and man (e.g. Saunders and Popovich 1978). Heritability estimates were originally formulated for the study of continuous variation, and the statistical difficulties accompanying their modification for binary data may decrease the validity of these family studies (Falconer 1981). Similarly, many so-called discrete traits do, in fact, show continuous variation (Corruccini 1974); subjectively constructed thresholds may not adequately express an underlying genetic basis.

Categorical scoring of traits has been adopted by many workers to increase the consistency of scoring, though the scores are usually dichotomised prior to analysis. The loss of information which accompanies dichotomisation is expressed as measurement error in the analysis. In heritability studies, this type of measurement error appears as environmental variance (Falconer 1981, p.124). This may account for the low heritability values in some studies, though why all studies are not affected is unclear. If this type of

error appears to reduce the genetic component of the trait data, it is possible that this accounts for anomalous results which are a frequent feature of non-metric population studies.

As stated by Richtsmeier and McGrath (1986):

> When dichotomizing, discrete categorization is imposed on a process which is, in fact, continuous. Since we cannot demonstrate the biological correctness of the chosen categories, lumping of trait expression may not reflect the biological bases of trait variation.

Since the methods of trait development are poorly comprehended, arbitrarily defined scoring thresholds can have no biological meaning. Richtsmeier and McGrath conclude that "until a fuller understanding of nonmetric trait etiology is developed, the promise of nonmetric traits will remain unfulfilled".

The differences between left and right sides also has genetic implications. If asymmetry is the result of *random* environmental noise, which at the moment seems to be the most commonly accepted theory, the difference in information in the sides is difficult to explain. It is quite possible that this difference is an artefact caused by inadequate sample size. If this is not the case, it suggests that 'sampling by individual', as advocated by Korey (1980) and Buikstra (1972) may be unwise, and that the 'additive genetic effects' theory of Berry and Berry (1967, R. J. Berry 1968, A. C. Berry 1975) and the 'genetic basis of asymmetry' theory of Ossenberg (1981) should be re-examined. Until this matter is resolved, it may be expedient to derive bilateral trait frequencies using one side only.

6.3. The biological shortcomings of the MMD formula.

It has been suggested that binary scoring of non-metric traits inadequately represents the underlying genetic factors, causing the MMDs derived from them to be poor indicators of population affinity. An alternative (or supplementary) explanation for the poor performance of discrete traits could lie in the mathematical shortcomings of the MMD formula.

Sjøvold (1973) thoroughly examines the mathematical implications of the Grewal-Smith MMD formula, and concludes that sample size could be a crucial factor. If the sample size is small, the variance of the transformed trait frequency (based on 1/N) may be artificially inflated. This may explain the lack of distinctiveness seen here between the

Greek sites. Sjøvold also notes that the weight of a variant in the MMD depends on the number of observations. Since weighting of the variables is in contrast to the principle of the angular transformation, the use of incomplete material in this study could mean that comparison of the MMDs between different groups is not strictly valid. Sjøvold further demonstrated that the variance of the MMD decreases if the number of traits used increases. It has already been noted that the subjective interpretation of the metric plots in chapter 5 is easier for the larger trait sets.

Despite these caveats, it is difficult to attribute the inconsistencies in the non-metric analyses of the 6 African groups entirely to inadequate sample size. Others have employed similar or smaller sample sizes (Berry & Berry 1967, Ossenberg 1976, Rothhammer et al. 1984), though the use of one side only for calculating of bilateral trait frequencies may effectively lower the sample size still further. It does, however, give equal weight to bilateral and midline traits, as recommended by Sjøvold (1973). Also, the 13 group, pooled-sex analyses still reveal the left/right inconsistency seen in the 6 group analyses, even though sample sizes are much increased.

At this point an assessment of the preliminary non-metric analysis is in order. This was undertaken so that unreliable traits should be excluded. Ossenberg (1976), among others, regards such a preliminary as essential, so that traits with a dubious genetic basis, scoring ambiguity, sex-linkage or inter-correlations are removed. The tests used here were successful in pinpointing the dubious traits, yet in the final assessment the plots based on all possible traits were the only ones from which group affinity could be easily read. Sjøvold (1973) stated that increasing both the number of traits and of observations decreased the variance of the MMD; it may be that in this study the moderate sample sizes mean that the number of traits is a critical feature. Yet to regard such preliminary screening as unnecessary (Berry (1975) thought that such 'unreliable' traits could safely be included since their effects would become 'diluted') may be unwise. This effect might be interpreted as empirical evidence that the MMD, like metric multivariate methods, is 'robust' to violations of its statistical assumptions. However, the evidence for robusticity of metric methods stems from the fact that, time and time again, reasonable results emerge, despite

despite using non-normal data. Considering the frequency of aberrant results in non-metric studies, the empirical evidence for robusticity seems paltry.

It could be argued that the shortcomings of discrete traits, as apparent here, might be overcome by use of a different statistic. Finnegan and Cooprider (1978), however, compared 13 different distance statistics and found very little difference among them. Included among the formulae tested are several gene-frequency statistics, some of which can accommodate multi-state variables, though (by implication) Finnegan and Cooprider used only binary data. Such a formula might be preferred if dichotomisation does indeed rob discrete traits of much of their genetic component (Richtsmeier and McGrath 1986). Even so, a gene frequency formula, designed for situations of multiple alleles at a single locus, may not be appropriate since the underlying genetic mechanism of these traits is meant to be polygenic (Grüneberg 1963).

Despite the superior performance of metric traits in this work, it should not be taken as advocating the abandonment of non-metric studies. In certain circumstances (e.g. where there is much distortion, or irreparable fragmentation of the crania) discrete traits may be all that is available. They are undoubtedly much quicker to record than measurements, even if accurate scoring is more difficult to attain than was at first thought. They do contain some genetic information, as several studies have shown, though further elucidations of their modes of development is needed before they can live up to their initial promise. Furthermore, several workers (Brothwell 1981, Corruccini 1974, Ossenberg 1976, Kaul et al. 1979) are of the opinion that they are only of use for studying relationships *within* major racial stocks. If this were the case, it would explain why many otherwise successful non-metric studies turn up the odd aberrant result. However, it is hoped that the present work will stimulate a renewed interest in craniometric analysis.

6.4. The implications of this work for metric studies.

Apart from its major findings, this study has several implications for the practical exercise of metric analysis. Most importantly, it emphasises the value of metric studies when sample sizes are small. The superior performance of metric distances, as presented in this

work, may derive more from the qualities of continuous near-normally distributed data, as compared to binary data, than any intrinsic genetic worth. As the preceding discussion shows, with binary data, sample sizes must be large before error-free distance statistics can be formulated. Where numbers are small, there is more information in continuous variables than in binary ones.

Discrete traits are said to be superior where remains are fragmentary. It is not a common archaeological finding, except perhaps in cremation sites, that a very large number of unreconstructable fragments are found. Usually at any one site, only a few dozen individuals are present, and with skill, enough reconstruction is possible to enable several measurements to be taken (Angel 1971).

In such a case, as this study has shown, several steps can be taken in metric analysis to maximise the information available in the sample. The pooling of the sexes seems to be justified, though caution is needed before samples with a greatly imbalanced sex-ratio are included. Similarly, the use of all possible data in calculating the means has allowed much better use of the information in the crania without giving unreasonable results. This method is not new; it has been used by Rao (1952), among others. It is only since the advent of modern electronic computers, and the reliance on packaged multivariate techniques, that complete data has been needed in metric analysis. By returning to these methods, where the emphasis is placed on determining taxonomic distance, before portrayal of the points, anthropometric research is once more coming under the umbrella of numerical taxonomy, which, one might suggest, is where it has always belonged.

6.5. Suggestions for further research.

This study suggests the following directions for research:

1 Efforts are needed to overcome the problems of measurement error in craniometry. The availability of electronic craniostats (which record co-ordinate points by means of positioning a mobile pointer (light-spot) onto an optically perfect reflection of the skull) now permit the taking of cranial measurements with negligible error. However, some of the traditional measurements (i.e. those recording maximum

dimensions rather than point to point distances) cannot be taken, and new ones (relating to discernable points) would need to be devised. Wherever possible, any new ones should be as similar to traditional measurements as possible, to aid comparison of data. Alternatively, the method of finite element analysis (as used by Cheverud et al. 1983) could be extended and applied to population studies, so that only a standard set of points would need to be defined.

2 Crania from Egypt and Greece should again be measured by a single person, using a single school of measurements, to confirm that the differences between Greek and Egyptian crania apparent in this work are not only due to different workers using different methods.

3 The theory of non-specificity is not universally accepted. Using the metric data recorded for several populations by W.W.Howells (1973), (currently available on computer at Bristol University, courtesy of Dr. J. H. Musgrave), Mahalanobis distances should be derived for several unique sets of measurements, and the different distance matrices compared.

4 More research in animals into the aetiology of non-metric traits is necessary, to establish which aspects are under genetic control, and which methods of recording them will most reflect the genetic components. If this reveals that only a categorical method of scoring will record the genetic aspect, methods of deriving a distance from such data must be investigated, or if necessary, new statistics formulated.

5 The correct method of determining frequencies for non-metric traits must be established. This involves the following projects:

a) Age effects must be documented, in many human populations, for as many traits as possible, so that the method of scoring by individual (which requires to know the directionality, if any, of the trait) can be compared with other methods.

b) Using several large (i.e. 200 or more in each group) populations, trait expression on the left and right side should be tested (as in this work), to see if

the information in each side differs. If this is the case, the theory of fluctuating asymmetry is brought under suspicion.

c) Following on from b), Ossenberg's (1981) contention, that the proportion of bilateral expressions increases as overall trait incidence rises, must be tested in many populations (and species). Only when it is known whether a double threshold or environmental noise determines left/right asymmetry can the correct method of recording frequencies be known.

Suggested samples for some of the above projects would include some recently discovered plague pit burials from the Old Royal Mint site, London, and the crania recovered from the wreck of the 'Mary Rose'. Such samples are preferable to interments from cemeteries, since the latter represent lineages, rather than populations in the biological sense, of which the plague-pits provide a superb example. Since the Black Death spread throughout Europe, contemporary populations from different sites should also be available.

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APPENDIX 1

TABLE A1.1.1

METRIC DATA - UNIVARIATE STATISTICS.

Glabello-occipital length (GOL).

MALE

Group	No.	Min.	Max.	Mean	SEM.	Var.	S.D.	Skew.	Kurt.
Sindos	12	169	195	184.67	2.36	66.97	8.18	(-)	(-)
Pieria	18	167	190	181.17	1.23	27.32	5.23	(-)	(+)*
Lerna	24	172	200	187.12	1.54	56.90	7.54	(+)	(-)
Athens-M	13	183	200	190.31	1.63	34.73	5.89	(+)	(-)**
Athens-G	14	175	193	183.29	1.50	31.60	5.62	(+)	(+)**
Fortetsa	6	173	191	186.00	2.71	44.00	6.63	(-)	(+)
Pyrgos	16	183	202	190.19	1.50	35.90	5.99	(+)	(+)
Giza	55	173	201	185.67	0.84	38.93	6.24	(+)	(+)***
Kerma	43	172	196	183.88	0.98	41.20	6.42	(+)	(+)
Naqada	50	165	199	184.14	0.97	47.31	6.88	(-)	(+)***
Sedment	39	167	195	182.00	0.99	37.84	6.15	(+)	(+)**
Badari	36	171	194	182.25	1.03	38.31	6.19	(+)	(+)
Teita	34	173	198	183.88	0.87	25.86	5.09	(+)	(+)***

FEMALE

Group	No.	Min.	Max.	Mean.	SEM.	Var.	S.D.	Skew.	Kurt.
Sindos	13	168	191	179.38	2.05	54.42	7.38	(+)	(-)
Pieria	8	168	189	174.00	2.39	45.71	6.76	(+)	(+)
Lerna	8	157	181	170.37	3.38	91.41	9.56	(-)	(-)
Athens-M	12	171	189	179.08	1.52	27.72	5.26	(+)	(-)**
Athens-G	2	175	178	176.50	1.50	4.50	2.12		
Fortetsa	5	167	180	177.00	2.51	31.50	5.61	(-)	(-)
Pyrgos	4	177	193	182.00	3.72	55.33	7.44	(+)	(+)
Giza	52	165	186	175.54	0.63	20.41	4.52	(+)	(+)***
Kerma	41	167	190	177.02	0.89	32.67	5.72	(+)	(+)
Naqada	51	167	189	177.31	0.75	28.38	5.33	(-)	(+)
Sedment	29	162	185	172.90	0.97	27.38	5.23	(+)	(+)***
Badari	22	169	185	176.95	0.88	17.00	4.12	(+)	(-)*
Teita	47	163	185	174.51	0.75	26.69	5.17	(-)	(+)**

(+) - positive skewness / kurtosis

(-) - negative skewness / kurtosis

*** - $p < 0.001$

** - $p < 0.01$

* - $p < 0.05$

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TABLE A1.1.2.

METRIC DATA - UNIVARIATE STATISTICS.

Basion-nasion length (BNL).

MALE

Group	No.	Min.	Max.	Mean	SEM.	Var.	S.D.	Skew.	Kurt.
Sindos	10	96	108	100.70	1.18	14.01	3.74	(+)	(+)
Pieria	16	95	108	101.37	0.87	12.12	3.48	(-)	(+)*
Lerna	16	97	117	105.75	1.43	32.73	5.72	(+)	(-)
Athens-M	10	96	105	100.60	0.98	9.60	3.10	(0)	(+)
Athens-G	11	96	107	102.45	1.15	14.67	3.83	(-)	(+)
Fortetsa	6	89	108	101.50	2.86	49.10	7.01	(-)	(-)
Pyrgos	7	96	106	101.00	1.57	17.33	4.16	(-)	(-)
Giza	55	93	110	101.42	0.49	13.40	3.66	(0)	(+)***
Kerma	43	93	113	101.42	0.61	16.06	4.01	(+)	(+)***
Naqada	50	87	113	99.60	0.76	28.78	5.36	(+)	(+)***
Sedment	36	94	110	100.92	0.73	18.94	4.35	(+)	(+)***
Badari	35	91	112	99.49	0.81	23.02	4.80	(+)	(+)***
Teita	34	96	111	102.24	0.62	13.28	3.64	(+)	(+)***

FEMALE

Group	No	Min	Max.	Mean.	SEM.	Var.	S.D.	Skew.	Kurt.
Sindos	10	93	109	98.90	1.55	24.10	4.91	(+)	(+)
Pieria	7	92	100	95.57	1.02	7.29	2.70	(+)	(-)**
Lerna	7	88	108	98.29	2.48	42.90	6.55	(-)	(-)
Athens-M	13	90	103	97.77	1.25	20.19	4.49	(-)	(-)
Athens-G	3	88	98	93.33	2.91	25.33	5.03	(-)	
Fortetsa	4	96	100	97.50	0.96	3.67	1.91	(+)	(+)***
Pyrgos	1	90	90	90.00	0.00	0.00	0.00		
Giza	52	90	105	95.92	0.46	11.05	3.32	(+)	(+)***
Kerma	41	90	102	95.93	0.55	12.22	3.50	(+)	(+)***
Naqada	51	84	106	94.76	0.55	15.42	3.93	(+)	(+)***
Sedment	29	86	104	94.83	0.73	15.43	3.93	(-)	(+)
Badari	22	91	103	96.32	0.80	14.23	3.77	(+)	(-)
Teita	47	90	102	96.43	0.46	9.95	3.15	(-)	(+)***

(+) - positive skewness / kurtosis

(-) - negative skewness / kurtosis

*** - $p < 0.001$

** - $p < 0.01$

* - $p < 0.05$

APPENDIX 1

TABLE A1.1.3.

METRIC DATA - UNIVARIATE STATISTICS.

Maximum cranial breadth (XCB).

MALE

Group	No.	Min.	Max.	Mean	SEM.	Var.	S.D.	Skew.	Kurt.
Sindos	11	135	152	143.91	1.49	24.49	4.95	(-)	(+)
Pieria	17	135	154	143.06	1.27	27.43	5.24	(+)	(+)*
Lerna	20	127	156	140.50	1.66	55.42	7.44	(+)	(-)
Athens-M	13	133	160	142.69	2.37	73.06	8.55	(+)	(-)
Athens-G	13	134	148	140.77	1.19	18.36	4.28	(-)	(+)***
Fortetsa	5	133	144	140.20	1.93	18.70	4.32	(-)	(+)
Pyrgos	17	132	146	139.12	1.01	17.36	4.17	(-)	(+)**
Giza	55	129	152	139.24	0.68	25.59	5.06	(+)	(+)**
Kerma	43	125	144	134.98	0.62	16.50	4.06	(-)	(+)**
Naqada	50	122	143	134.26	0.64	20.73	4.55	(-)	(+)***
Sedment	39	130	147	138.44	0.67	17.25	4.15	(-)	(+)***
Badari	36	122	140	130.94	0.77	21.08	4.59	(-)	(+)
Teita	34	119	138	129.85	0.73	18.13	4.26	(-)	(+)

FEMALE

Group	No.	Min.	Max.	Mean	SEM.	Var.	S.D.	Skew.	Kurt.
Sindos	10	133	152	141.50	1.87	34.94	5.91	(+)	(+)
Pieria	8	133	151	140.12	1.82	26.41	5.14	(+)	(+)
Lerna	9	127	147	135.56	2.53	57.78	7.60	(+)	(-)
Athens-M	14	128	144	136.07	1.08	16.23	4.03	(-)	(+)***
Athens-G	4	134	144	139.25	2.29	20.92	4.57	(-)	(-)
Fortetsa	4	131	141	135.75	2.14	18.25	4.27	(+)	(-)
Pyrgos	3	136	146	141.33	2.91	25.33	5.03	(-)	
Giza	52	127	144	135.58	0.61	19.39	4.40	(-)	(+)***
Kerma	41	122	140	130.76	0.67	18.19	4.26	(-)	(+)***
Naqada	51	122	141	131.76	0.59	17.54	4.19	(+)	(+)***
Sedment	29	123	146	133.45	1.08	33.90	5.82	(+)	(+) ***
Badari	21	122	139	130.57	0.94	18.46	4.30	(-)	(+)
Teita	47	116	139	126.23	0.64	19.05	4.36	(+)	(+)***

(+) - positive skewness / kurtosis

(-) - negative skewness / kurtosis

*** - $p < 0.001$

** - $p < 0.01$

* - $p < 0.05$

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TABLE A1.1.4.

METRIC DATA - UNIVARIATE STATISTICS.

Bizygomatic breadth (ZYB).

MALE

Group	No.	Min.	Max.	Mean	SEM.	Var.	S.D.	Skew.	Kurt.
Sindos	12	117	142	131.00	1.93	44.55	6.67	(-)	(+)
Pieria	17	123	145	132.41	1.40	33.13	5.76	(+)	(+)
Lerna	22	116	144	130.18	1.64	58.82	7.67	(-)	(-)
Athens-M	10	118	136	127.80	1.60	25.73	5.07	(-)	(+)
Athens-G	13	123	148	131.92	2.04	54.24	7.37	(+)	(+)
Fortetsa	4	121	140	133.25	4.21	70.92	8.42	(-)	(-)
Pyrgos	5	117	134	125.80	2.76	38.20	6.18	(-)	(-)
Giza	55	121	135	128.69	0.58	18.37	4.29	(-)	(+)***
Kerma	43	113	137	127.88	0.77	25.30	5.03	(-)	(+)***
Naqada	50	113	143	125.18	0.78	30.64	5.54	(+)	(+)*
Sedment	28	117	138	127.36	0.94	24.61	4.96	(-)	(+)**
Badari	32	110	133	122.72	0.88	24.85	4.99	(-)	(+)*
Teita	34	123	143	131.00	0.71	16.97	4.12	(+)	(+)***

FEMALE

Group	No.	Min.	Max.	Mean	SEM.	Var.	S.D.	Skew.	Kurt.
Sindos	11	113	136	123.09	1.96	42.09	6.49	(+)	(-)
Pieria	6	121	129	124.83	1.11	7.37	2.71	(+)	(+)
Lerna	9	118	133	122.78	1.72	26.69	5.17	(+)	(-)
Athens-M	12	116	127	122.33	1.05	13.33	3.65	(-)	(+)
Athens-G	2	120	122	121.00	1.00	2.00	1.41		
Fortetsa	2	123	123	123.00	0.00	0.00	0.00		
Pyrgos	1	113	113	113.00					
Giza	52	113	128	120.12	0.47	11.55	3.40	(+)	(+)***
Kerma	41	109	127	119.98	0.64	16.57	4.07	(-)	(+)***
Naqada	51	112	128	118.88	0.55	15.63	3.95	(+)	(+)***
Sedment	24	106	125	117.58	0.96	22.17	4.71	(-)	(+)***
Badari	13	110	132	117.85	1.53	30.31	5.51	(+)	(+)
Teita	47	117	137	124.06	0.58	15.93	3.99	(+)	(+)***

(+) - positive skewness / kurtosis

(-) - negative skewness / kurtosis

*** - $p < 0.001$

** - $p < 0.01$

* - $p < 0.05$

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TABLE A1.1.5.

METRIC DATA - UNIVARIATE STATISTICS.

Nasion-prosthion height (NPH).

MALE

Group	No.	Min.	Max	Mean	SEM.	Var	S.D.	Skew.	Kurt.
Sindos	12	65	79	71.25	1.48	26.39	5.14	(+)	(-)
Pieria	15	57	75	65.27	1.11	18.64	4.32	(+)	(+)
Lerna	23	61	71	66.09	0.62	8.90	2.98	(-)	(-)
Athens-M	8	63	72	67.25	1.25	12.50	3.54	(+)	(-)
Athens-G	10	60	70	65.40	1.06	11.16	3.34	(-)	(-)
Fortetsa	4	63	69	66.25	1.38	7.58	2.75	(-)	(-)
Pyrgos	6	62	69	67.17	1.08	6.97	2.64	(-)	(-)
Giza	55	60	77	68.42	0.39	8.58	2.93	(-)	(+)*
Kerma	43	61	78	68.81	0.64	17.54	4.19	(+)	(-)
Naqada	50	57	78	67.90	0.65	21.19	4.60	(-)	(-)
Sedment	37	62	81	71.51	0.70	18.15	4.26	(-)	(-)
Badari	34	59	74	67.15	0.68	15.89	3.99	(-)	(-)
Teita	34	59	74	66.00	0.68	15.52	3.94	(+)	(-)

FEMALE

Group	No	Min	Max	Mean	SEM.	Var	S.D.	Skew.	Kurt.
Sindos	4	65	68	66.50	0.65	1.67	1.29	(0)	(+)
Pieria	6	59	69	64.50	1.48	13.10	3.62	(-)	(-)
Lerna	9	57	67	61.33	1.01	9.25	3.04	(+)	(-)
Athens-M	12	58	71	63.00	1.30	20.18	4.49	(+)	(-)
Athens-G	3	56	66	60.67	2.91	25.33	5.03	(+)	
Fortetsa	1	64	64	64.00	0.00	0.00	0.00		
Pyrgos	0								
Giza	52	57	70	64.13	0.46	11.06	3.33	(-)	(-)
Kerma	41	61	75	66.54	0.49	9.65	3.11	(+)	(-)
Naqada	51	59	74	65.67	0.50	12.59	3.55	(+)	(-)
Sedment	28	55	74	67.14	0.78	17.16	4.14	(-)	(+)
Badari	20	58	76	64.75	0.99	19.78	4.45	(+)	(+)
Teita	47	52	72	61.06	0.63	18.63	4.32	(+)	(-)

(+) - positive skewness / kurtosis

(-) - negative skewness / kurtosis

*** - $p < 0.001$

** - $p < 0.01$

* - $p < 0.05$

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TABLE A1.1.6.

METRIC DATA - UNIVARIATE STATISTICS.

Nasal height (NLH).

MALE

Group	No.	Min.	Max.	Mean	SEM.	Var	S.D.	Skew.	Kurt.
Sindos	13	46	57	52.23	1.03	13.86	3.72	(-)	(-)
Pieria	15	43	56	50.73	0.91	12.50	3.53	(-)	(+)
Lerna	22	46	57	50.68	0.57	7.18	2.68	(+)	(+)
Athens-M	8	47	53	50.75	0.73	4.21	2.05	(-)	(+)
Athens-G	10	46	55	50.80	0.73	5.29	2.30	(-)	(+)
Fortetsa	4	52	54	52.75	0.48	0.92	0.96	(+)	(+)**
Pyrgos	6	44	53	50.33	1.45	12.67	3.56	(-)	(-)
Giza	55	44	57	51.73	0.36	7.31	2.70	(-)	(+)
Kerma	43	44	60	49.88	0.48	10.11	3.18	(+)	(+)
Naqada	50	42	56	49.40	0.43	9.10	3.02	(-)	(-)
Sedment	37	43	57	52.08	0.52	10.08	3.17	(-)	(+)
Badari	34	43	53	48.44	0.47	7.47	2.73	(-)	(-)
Teita	34	43	58	50.09	0.48	7.84	2.80	(+)	(+)

FEMALE

Group	No.	Min.	Max.	Mean	SEM.	Var	S.D.	Skew.	Kurt.
Sindos	5	50	60	52.20	1.96	19.20	4.38	(+)	(+)
Pieria	6	47	52	49.00	0.73	3.20	1.79	(+)	(-)
Lerna	9	42	50	46.11	1.06	10.11	3.18	(+)	(-)
Athens-M	12	42	55	47.83	1.18	16.70	4.09	(+)	(-)
Athens-G	3	42	46	44.67	1.33	5.33	2.31	(-)	
Fortetsa	1	49	49	49.00					
Pyrgos	0								
Giza	52	43	55	48.98	0.32	5.23	2.29	(-)	(+)
Kerma	41	43	52	47.39	0.37	5.74	2.40	(+)	(-)
Naqada	51	40	51	46.92	0.39	7.71	2.78	(-)	(+)
Sedment	28	41	54	48.50	0.49	6.78	2.60	(-)	(+)
Badari	20	41	51	45.65	0.64	8.13	2.85	(+)	(-)
Teita	47	40	53	46.49	0.48	10.82	3.29	(-)	(-)

(+) - positive skewness / kurtosis

(-) - negative skewness / kurtosis

*** - $p < 0.001$

** - $p < 0.01$

* - $p < 0.05$

APPENDIX 1

TABLE A1.1.7.

METRIC DATA - UNIVARIATE STATISTICS.

Orbital height (OBH).

MALE

Group	No.	Min.	Max	Mean	SEM.	Var	S.D.	Skew.	Kurt.
Sindos	12	30	38	33.83	0.72	6.15	2.48	(-)	(-)
Pieria	15	29	35	31.20	0.44	2.89	1.70	(+)	(-)
Lerna	23	27	38	31.83	0.48	5.24	2.29	(+)	(+)
Athens-M	11	30	36	33.73	0.59	3.82	1.95	(-)	(-)
Athens-G	12	31	34	32.67	0.33	1.33	1.15	(-)	(-)
Fortetsa	4	31	34	33.00	0.71	2.00	1.41	(-)	(-)
Pyrgos	7	32	37	34.00	0.65	3.00	1.73	(+)	(-)
Giza	55	29	39	32.98	0.27	4.13	2.03	(+)	(+)
Kerma	43	29	41	32.98	0.34	5.07	2.25	(+)*	(+)**
Naqada	50	29	37	32.62	0.32	5.14	2.27	(+)	(-)
Sedment	36	29	37	33.61	0.32	3.67	1.92	(-)	(-)
Badari	33	28	37	32.18	0.34	3.90	1.98	(+)	(+)
Teita	34	29	36	33.29	0.32	3.43	1.85	(-)	(-)

FEMALE

Group	No.	Min.	Max.	Mean	SEM.	Var	S.D.	Skew.	Kurt.
Sindos	6	33	37	34.67	0.56	1.87	1.37	(+)	(-)
Pieria	6	30	33	31.33	0.61	2.27	1.51	(+)	(-)
Lerna	11	26	37	32.00	0.93	9.60	3.10	(-)	(-)
Athens-M	13	29	38	32.77	0.79	8.19	2.86	(+)	(-)
Athens-G	2	31	33	32.00	1.00	2.00	1.41		
Fortetsa	2	32	37	34.50	2.50	12.50	3.54		
Pyrgos	1	28	28	28.00					
Giza	52	27	36	32.75	0.24	3.01	1.74	(-)	(+)
Kerma	41	29	37	32.68	0.33	4.57	2.14	(+)	(-)
Naqada	51	27	38	32.31	0.30	4.58	2.14	(-)	(+)
Sedment	28	29	36	32.71	0.37	3.84	1.96	(-)	(-)
Badari	18	29	35	31.33	0.46	3.76	1.94	(+)	(-)
Teita	47	29	37	32.15	0.27	3.39	1.84	(+)	(+)

(+) - positive skewness / kurtosis

(-) - negative skewness / kurtosis

*** - $p < 0.001$
** - $p < 0.01$
* - $p < 0.05$

APPENDIX 1

TABLE A1.1.8.

METRIC DATA - UNIVARIATE STATISTICS.

Orbital breadth (OBB).

MALE

Group	No.	Min.	Max.	Mean	SEM.	Var.	S.D.	Skew.	Kurt.
Sindos	13	36	41	38.69	0.50	3.23	1.80	(-)	(-)
Pieria	15	37	43	39.73	0.40	2.35	1.53	(+)	(-)
Lerna	25	37	42	39.32	0.26	1.64	1.28	(+)	(-)**
Athens-M	11	35	41	38.36	0.62	4.25	2.06	(-)	(-)
Athens-G	12	38	44	40.58	0.54	3.54	1.88	(+)	(-)
Fortetsa	4	40	43	40.75	0.75	2.25	1.50	(+)	(+)
Pyrgos	7	35	41	38.43	0.95	6.29	2.51	(-)	(-)
Giza	55	35	44	39.42	0.24	3.06	1.75	(+)	(-)
Kerma	43	38	45	41.63	0.25	2.76	1.66	(-)	(-)*
Naqada	50	38	49	42.94	0.33	5.49	2.34	(+)	(-)
Sedment	35	38	47	41.86	0.39	5.24	2.29	(+)	(-)
Badari	34	37	44	40.03	0.28	2.76	1.66	(+)	(-)
Teita	34	37	43	39.65	0.26	2.36	1.54	(+)	(-)

FEMALE

Group	No.	Min.	Max.	Mean	SEM.	Var	S.D.	Skew.	Kurt.
Sindos	5	37	42	39.40	0.81	3.30	1.82	(+)	(-)
Pieria	6	37	40	38.17	0.48	1.37	1.17	(+)	(-)
Lerna	11	34	40	37.45	0.56	3.47	1.86	(-)	(-)
Athens-M	13	34	40	37.08	0.43	2.41	1.55	(-)	(-)
Athens-G	2	37	38	37.50	0.50	0.50	0.71		
Fortetsa	2	39	40	39.50	0.50	0.50	0.71		
Pyrgos	0								
Giza	52	35	42	37.83	0.22	2.54	1.59	(+)	(-)
Kerma	41	37	46	40.19	0.27	3.06	1.75	(+)	(+)*
Naqada	51	36	46	41.63	0.32	5.08	2.25	(-)	(+)
Sedment	28	36	44	39.82	0.41	4.67	2.16	(-)	(-)
Badari	18	37	43	39.39	0.35	2.25	1.50	(+)	(-)
Teita	47	34	41	37.74	0.22	2.24	1.50	(-)	(-)

(+) - positive skewness / kurtosis

(-) - negative skewness / kurtosis

*** - $p < 0.001$
** - $p < 0.01$
* - $p < 0.05$

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TABLE A1.1.9.

METRIC DATA - UNIVARIATE STATISTICS.

Nasal breadth (NLB).

MALE

Group	No.	Min.	Max.	Mean	SEM.	Var	S.D.	Skew.	Kurt.
Sindos	12	23	28	25.08	0.48	2.81	1.68	(+)	(-)
Pieria	15	21	30	24.33	0.58	5.10	2.26	(+)	(+)
Lerna	21	21	29	25.00	0.46	4.40	2.10	(+)	(-)
Athens-M	8	22	25	23.62	0.38	1.13	1.06	(+)	(-)
Athens-G	8	22	25	23.62	0.50	1.98	1.41	(-)	(-)
Fortetsa	4	26	30	28.25	0.85	2.92	1.71	(-)	(-)
Pyrgos	4	19	24	22.50	1.19	5.67	2.38	(-)	(-)
Giza	55	22	29	24.82	0.23	3.00	1.73	(+)	(+)
Kerma	43	23	30	25.84	0.28	3.33	1.82	(+)	(-)
Naqada	50	22	30	25.30	0.26	3.44	1.85	(+)	(-)
Sedment	38	21	28	24.58	0.31	3.55	1.88	(-)	(-)
Badari	34	22	28	25.00	0.28	2.67	1.63	(+)	(-)
Teita	34	25	32	27.91	0.31	3.23	1.80	(+)	(-)

FEMALE

Group	No.	Min.	Max.	Mean	SEM.	Var	S.D.	Skew.	Kurt.
Sindos	5	20	24	23.20	0.80	3.20	1.79	(-)	(+)
Pieria	6	23	26	24.50	0.43	1.10	1.05	(+)	(-)
Lerna	11	21	25	22.64	0.36	1.45	1.21	(+)	(-)
Athens-M	11	18	25	22.36	0.74	6.05	2.46	(-)	(-)
Athens-G	1	22	22	22.00					
Fortetsa	2	20	24	22.00	2.00	8.00	2.83		
Pyrgos	0								
Giza	52	21	28	24.02	0.22	2.49	1.58	(+)	(-)
Kerma	41	20	28	24.93	0.30	3.62	1.90	(-)	(-)
Naqada	51	21	29	24.47	0.24	2.93	1.71	(+)	(-)
Sedment	28	21	27	23.82	0.32	2.89	1.70	(+)	(-)
Badari	20	22	26	23.65	0.24	1.19	1.09	(-)	(-)
Teita	47	24	31	27.32	0.26	3.18	1.78	(+)	(-)

(+) - positive skewness / kurtosis

(-) - negative skewness / kurtosis

*** - $p < 0.001$

** - $p < 0.01$

* - $p < 0.05$

APPENDIX 1

TABLE A1.1.10.

METRIC DATA - UNIVARIATE STATISTICS.

Bimaxillary breadth (ZMB).

MALE

Group	No.	Min.	Max.	Mean	SEM.	Var	S.D.	Skew.	Kurt.
Sindos	12	85	102	93.00	1.30	20.36	4.51	(+)	(-)
Pieria	14	87	108	93.86	1.65	38.29	6.19	(+)	(+)
Lerna	21	86	109	96.90	1.39	40.79	6.39	(+)	(-)
Athens-M	7	82	96	91.57	1.72	20.62	4.54	(-)	(+)
Athens-G	12	85	102	93.50	1.72	35.55	5.96	(+)	(-)
Fortetsa	3	93	103	97.33	2.96	26.33	5.13	(+)	
Pyrgos	6	85	92	88.67	1.15	7.87	2.80	(-)	(-)*
Giza	55	83	103	93.87	0.59	18.93	4.35	(-)	(+)***
Kerma	43	88	103	95.33	0.59	15.08	3.88	(+)	(+)***
Naqada	50	85	110	95.82	0.84	34.89	5.91	(+)	(+)
Sedment	36	87	103	94.03	0.82	24.14	4.91	(+)	(+)
Badari	34	82	107	94.65	0.88	26.17	5.12	(+)	(+)*
Teita	34	88	110	99.35	0.90	27.75	5.27	(+)	(+)

FEMALE

Group	No.	Min.	Max.	Mean	SEM.	Var	S.D.	Skew.	Kurt.
Sindos	5	86	95	91.20	1.59	12.70	3.56	(-)	(-)
Pieria	6	90	98	93.50	1.50	13.50	3.67	(+)	(-)
Lerna	10	79	94	87.90	1.51	22.77	4.77	(-)	(-)
Athens-M	9	81	94	87.78	1.69	25.69	5.07	(-)	(-)
Athens-G	2	86	92	89.00	3.00	18.00	4.24		
Fortetsa	2	89	89	89.00	0.00	0.00	0.00		
Pyrgos	0								
Giza	52	80	98	89.48	0.66	22.80	4.78	(+)	(+)**
Kerma	41	83	101	92.00	0.73	21.85	4.67	(-)	(+)*
Naqada	51	83	101	92.88	0.60	18.51	4.30	(-)	(+)***
Sedment	27	81	98	89.48	0.77	16.03	4.00	(+)	(+)
Badari	18	83	97	89.56	0.91	14.97	3.87	(+)	(-)
Teita	47	82	103	93.81	0.67	21.07	4.59	(-)	(+)**

(+) - positive skewness / kurtosis

(-) - negative skewness / kurtosis

*** - $p < 0.001$

** - $p < 0.01$

* - $p < 0.05$

APPENDIX 1

TABLE A1.2.1.

ANALYSIS OF VARIANCE OF CRANIAL MEASUREMENTS IN 13 GROUPS.

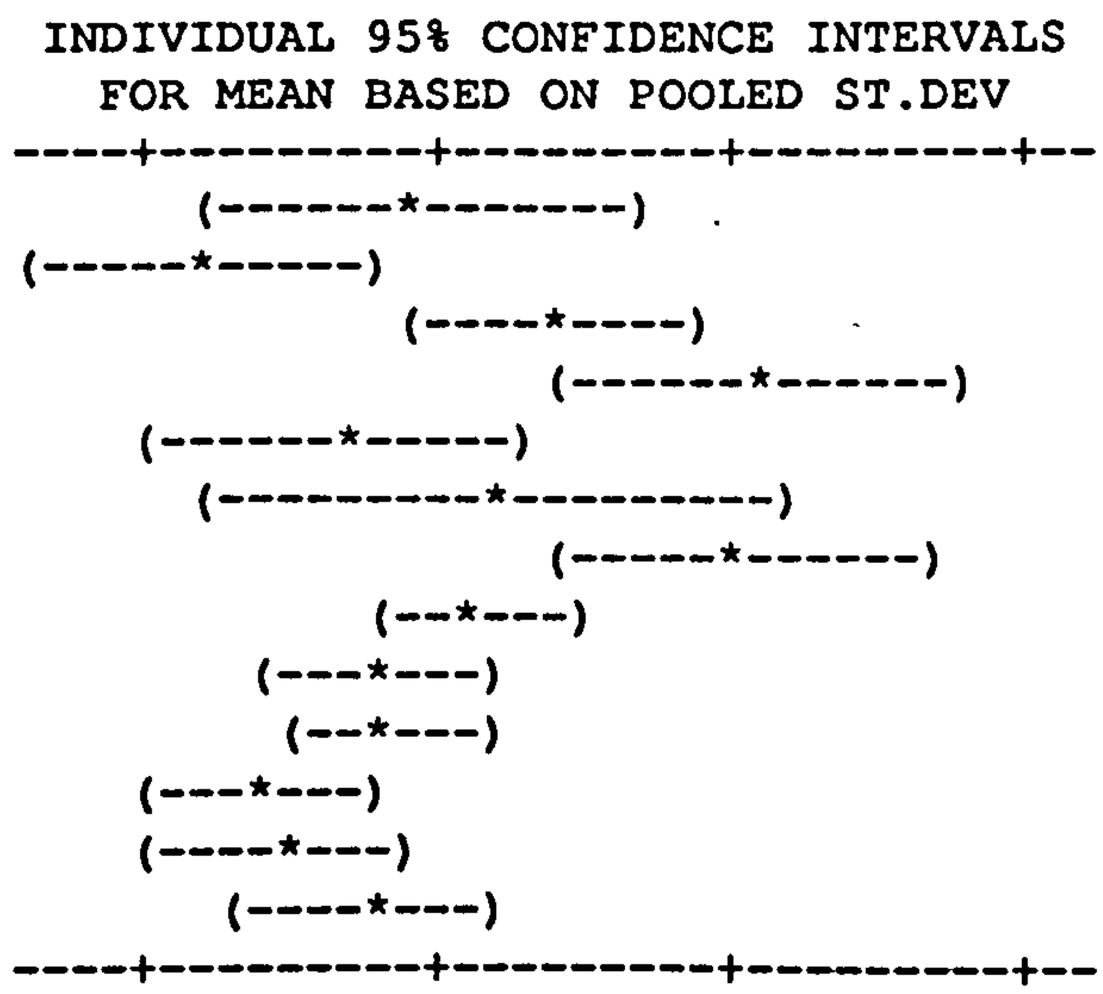
Glabello-Occipital Length (GOL)

MALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	12	1892.6	157.7	3.94
WITHIN-GROUP	347	13878.7	40.0	
TOTAL	359	15771.3		

GROUP	N	MEAN	ST.DEV
Sindos	12	184.67	8.18
Pieria	18	181.17	5.23
Lerna	24	187.13	7.54
Athens-M	13	190.31	5.89
Athens-G	14	183.29	5.62
Fortetsa	6	186.00	6.63
Pyrgos	16	190.19	5.99
Giza	55	185.67	6.24
Kerma	43	183.88	6.42
Naqada	50	184.14	6.88
Sedment	39	182.00	6.15
Badari	36	182.25	6.19
Teita	34	183.88	5.09

POOLED ST.DEV = 6.32

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV



FEMALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	11	1242.8	113.0	3.80
WITHIN-GROUP	280	8328.1	29.7	
TOTAL	291	9570.9		

GROUP	N	MEAN	ST.DEV
Sindos	13	179.38	7.38
Pieria	8	174.00	6.76
Lerna	8	170.38	9.56
Athens-M	12	179.08	5.26
Athens-G			
Fortetsa	5	177.00	5.61
Pyrgos	4	182.00	7.44
Giza	52	175.54	4.52
Kerma	41	177.02	5.72
Naqada	51	177.31	5.33
Sedment	29	172.90	5.23
Badari	22	176.95	4.12
Teita	47	174.51	5.17

POOLED ST.DEV = 5.45

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV

APPENDIX 1

TABLE A1.2.2.

ANALYSIS OF VARIANCE OF CRANIAL MEASUREMENTS IN 13 GROUPS.

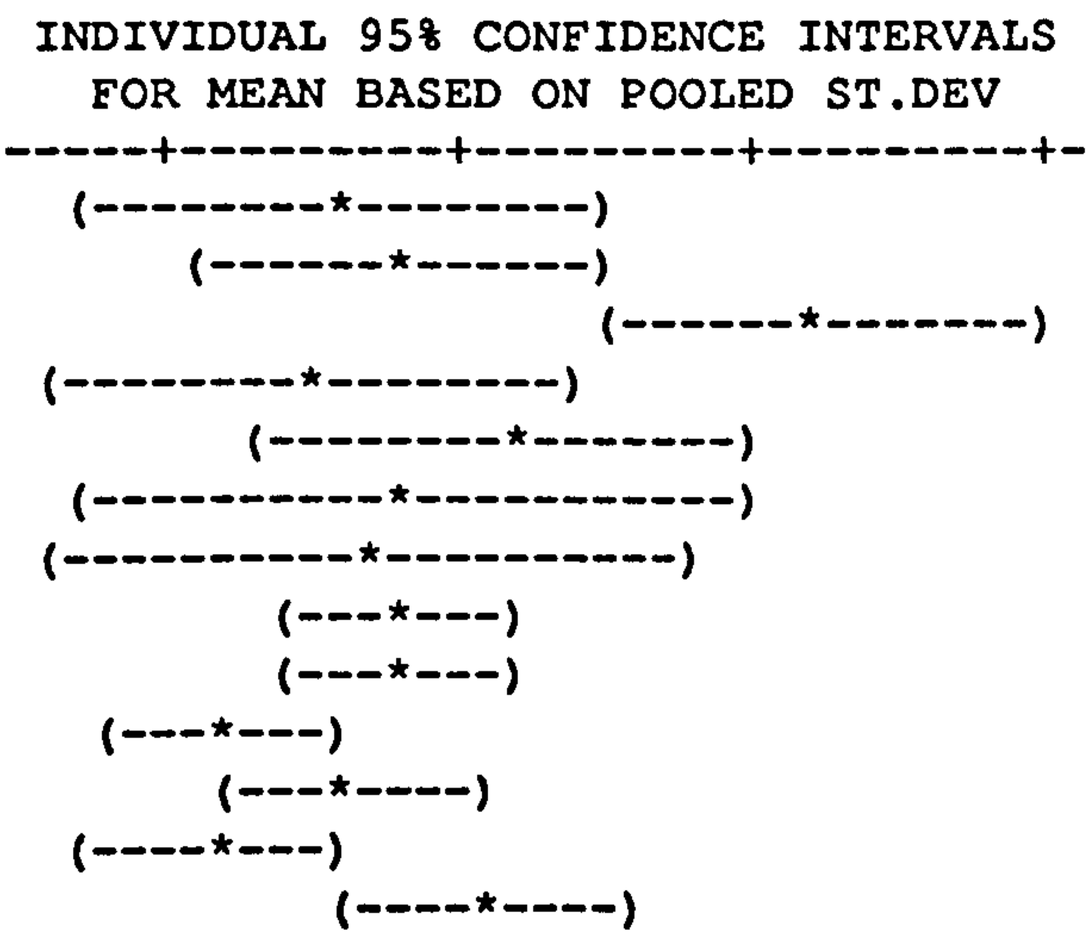
Basion-Nasion Length (BNL)

MALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	12	630.2	52.5	2.73
WITHIN-GROUP	316	6072.9	19.2	
TOTAL	328	6703.1		

GROUP	N	MEAN	ST.DEV
Sindos	10	100.70	3.74
Pieria	16	101.37	3.48
Lerna	16	105.75	5.72
Athens-M	10	100.60	3.10
Athens-G	11	102.45	3.83
Fortetsa	6	101.50	7.01
Pyrgos	7	101.00	4.16
Giza	55	101.42	3.66
Kerma	43	101.42	4.01
Naqada	50	99.60	5.36
Sedment	36	100.92	4.35
Badari	35	99.49	4.80
Teita	34	102.24	3.64

POOLED ST.DEV = 4.38

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV

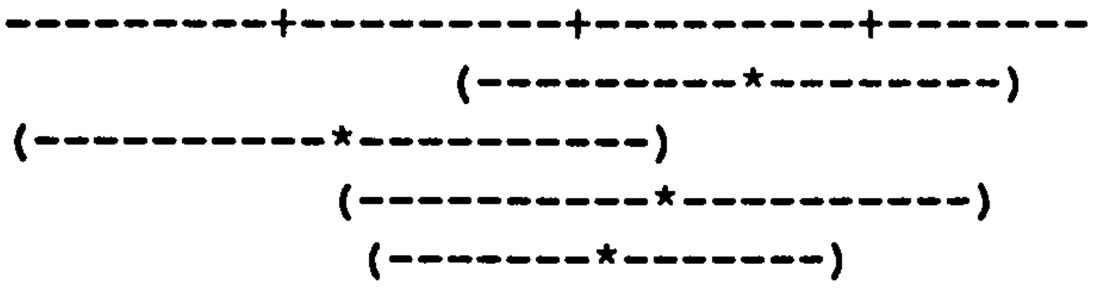


FEMALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	10	300.5	30.0	2.16
WITHIN-GROUP	272	3783.4	13.9	
TOTAL	282	4083.9		

GROUP	N	MEAN	ST.DEV
Sindos	10	98.90	4.91
Pieria	7	95.57	2.70
Lerna	7	98.29	6.55
Athens-M	13	97.77	4.49
Athens-G			
Fortetsa	4	97.50	1.91
Pyrgos			
Giza	52	95.92	3.32
Kerma	41	95.93	3.50
Naqada	51	94.76	3.93
Sedment	29	94.83	3.93
Badari	22	96.32	3.77
Teita	47	96.43	3.15

POOLED ST.DEV = 3.73

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV



APPENDIX 1

TABLE A1.2.3.

ANALYSIS OF VARIANCE OF CRANIAL MEASUREMENTS IN 13 GROUPS.

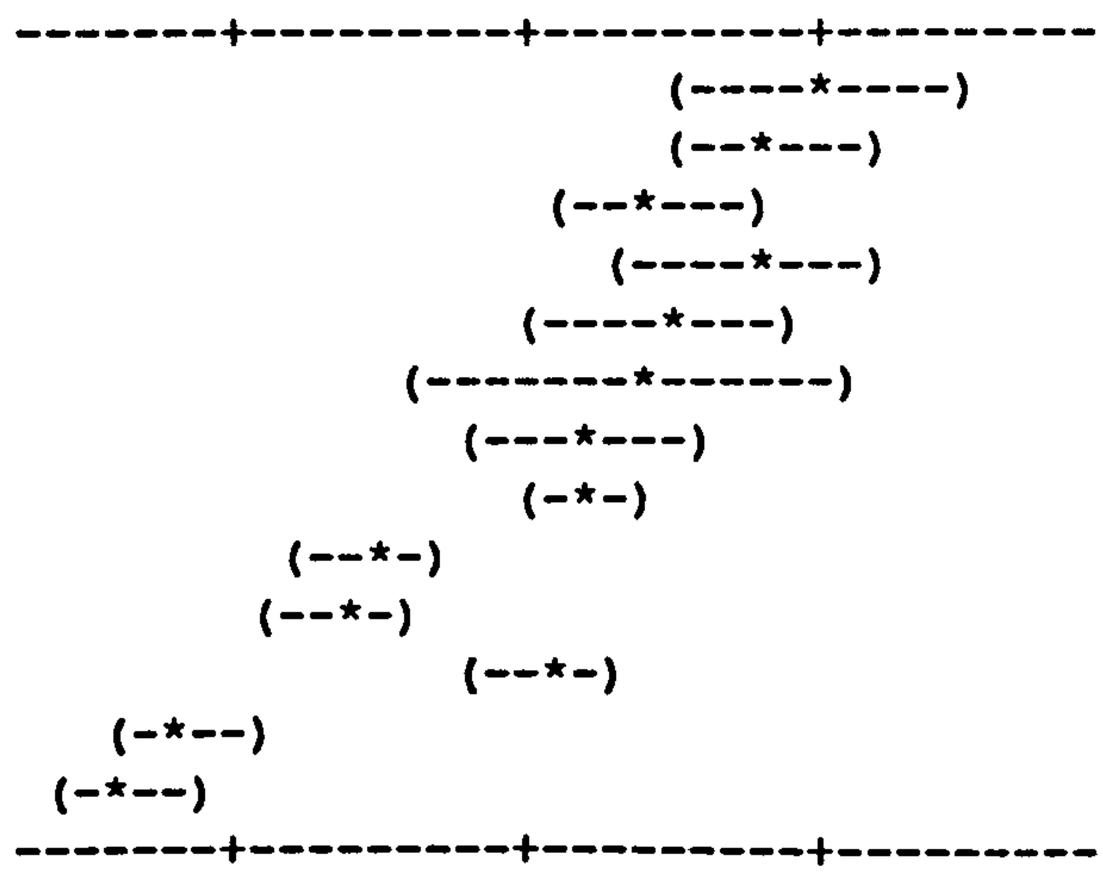
Maximum Cranial Breadth (XCB)

MALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	12	6072.2	506.0	20.81
WITHIN-GROUP	340	8268.8	24.3	
TOTAL	352	14341.0		

GROUP	N	MEAN	ST.DEV
Sindos	11	143.91	4.95
Pieria	17	143.06	5.24
Lerna	20	140.50	7.44
Athens-M	13	142.69	8.55
Athens-G	13	140.77	4.28
Fortetsa	5	140.20	4.32
Pyrgos	17	139.12	4.17
Giza	55	139.24	5.06
Kerma	43	134.98	4.06
Naqada	50	134.26	4.55
Sedment	39	138.44	4.15
Badari	36	130.94	4.59
Teita	34	129.85	4.26

POOLED ST.DEV = 4.93

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV

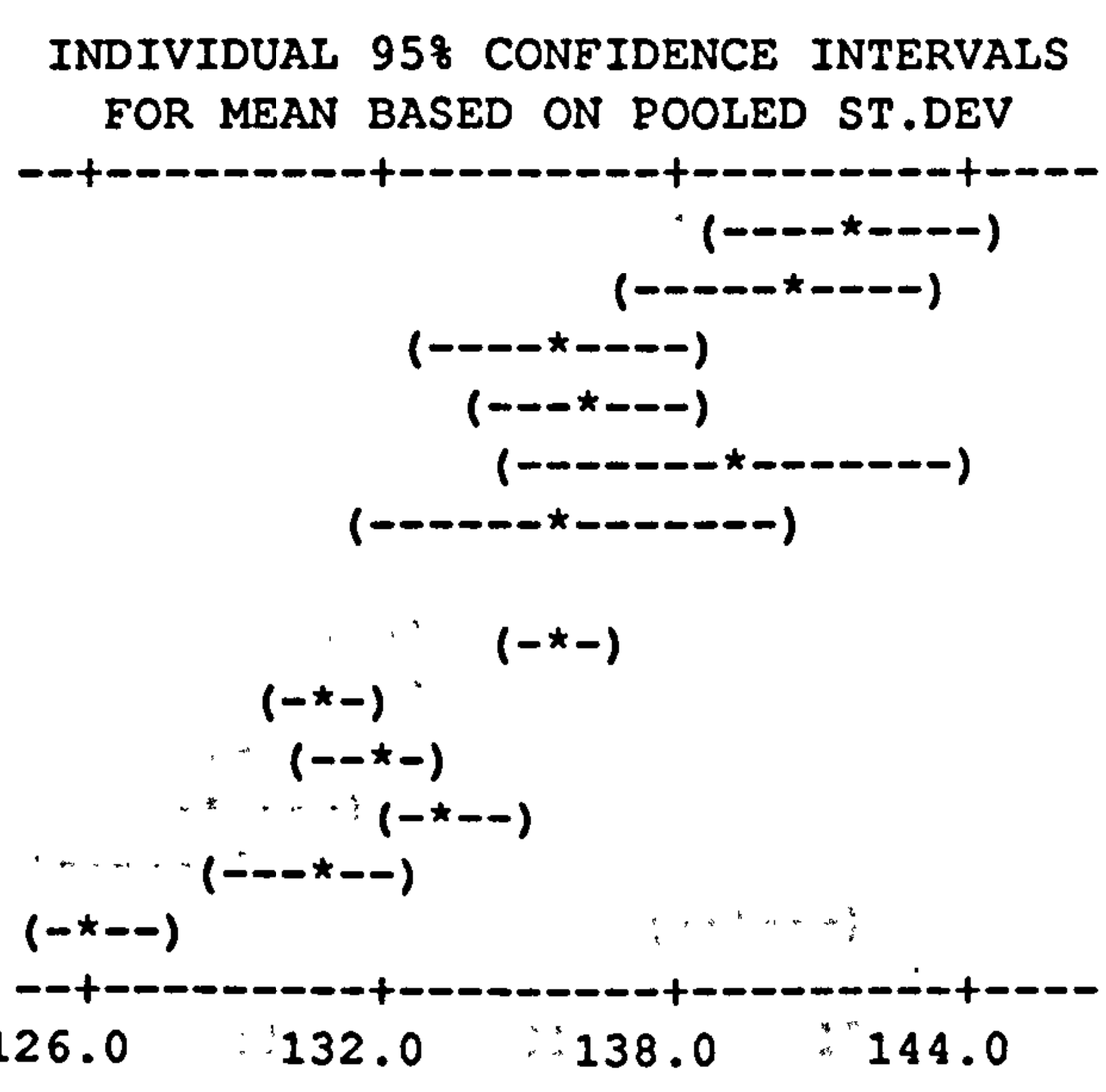


FEMALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	11	4355.8	396.0	18.11
WITHIN-GROUP	278	6078.2	21.9	
TOTAL	289	10434.0		

GROUP	N	MEAN	ST.DEV
Sindos	10	141.50	5.91
Pieria	8	140.13	5.14
Lerna	9	135.56	7.60
Athens-M	14	136.07	4.03
Athens-G	4	139.25	4.57
Fortetsa	4	135.75	4.27
Pyrgos			
Giza	52	135.58	4.40
Kerma	41	130.76	4.26
Naqada	51	131.76	4.19
Sedment	29	133.45	5.82
Badari	21	130.57	4.30
Teita	47	126.23	4.36

POOLED ST.DEV = 4.68

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV



APPENDIX 1

TABLE A1.2.4.

ANALYSIS OF VARIANCE OF CRANIAL MEASUREMENTS IN 13 GROUPS.

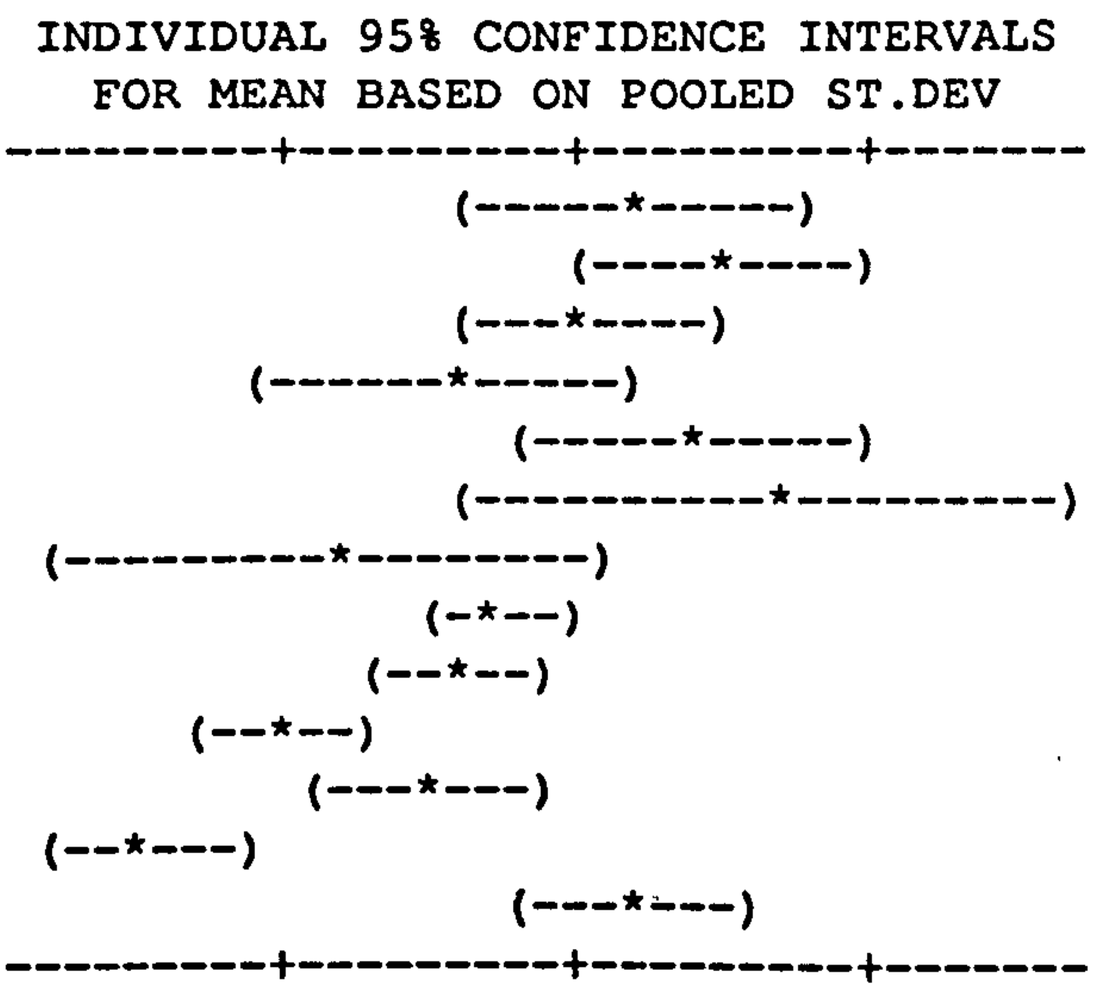
Bizygomatic Breadth (ZYB)

MALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	12	2511.2	209.3	7.21
WITHIN-GROUP	312	9053.9	29.0	
TOTAL	324	11565.1		

GROUP	N	MEAN	ST.DEV
Sindos	12	131.00	6.67
Pieria	17	132.41	5.76
Lerna	22	130.18	7.67
Athens-M	10	127.80	5.07
Athens-G	13	131.92	7.37
Fortetsa	4	133.25	8.42
Pyrgos	5	125.80	6.18
Giza	55	128.69	4.29
Kerma	43	127.88	5.03
Naqada	50	125.18	5.54
Sedment	28	127.36	4.96
Badari	32	122.72	4.99
Teita	34	131.00	4.12

POOLED ST.DEV = 5.39

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV

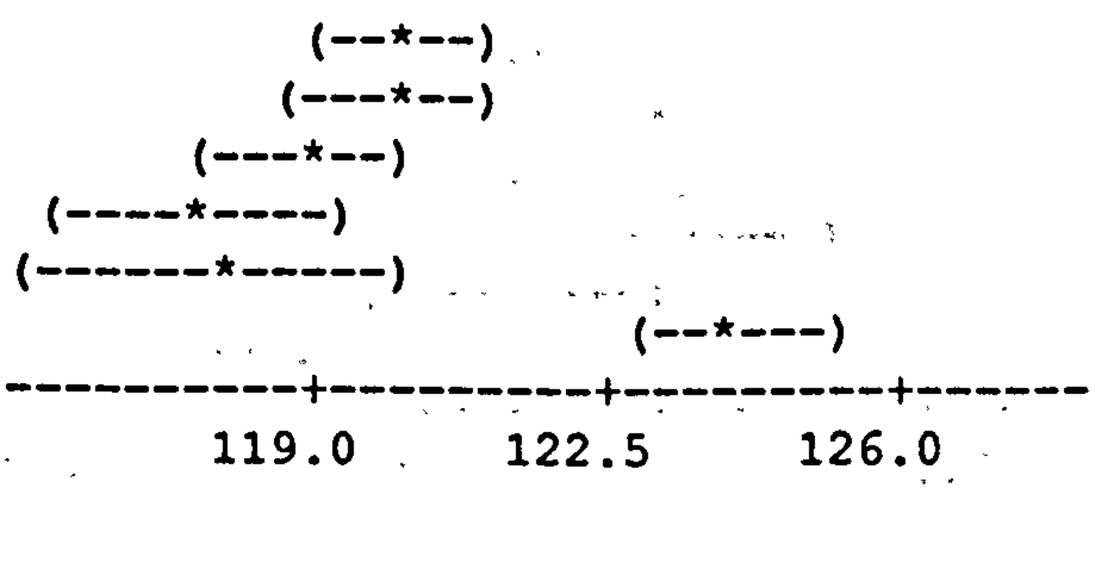


FEMALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	9	1313.8	146.0	8.38
WITHIN-GROUP	256	4457.9	17.4	
TOTAL	265	5771.6		

GROUP	N	MEAN	ST.DEV
Sindos	11	123.09	6.49
Pieria	6	124.83	2.71
Lerna	9	122.78	5.17
Athens-M	12	122.33	3.65
Athens-G			
Fortetsa			
Pyrgos			
Giza	52	120.12	3.40
Kerma	41	119.98	4.07
Naqada	51	118.88	3.95
Sedment	24	117.58	4.71
Badari	13	117.85	5.51
Teita	47	124.06	3.99

POOLED ST.DEV = 4.17

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV



APPENDIX 1

TABLE A1.2.5.

ANALYSIS OF VARIANCE OF CRANIAL MEASUREMENTS IN 13 GROUPS.

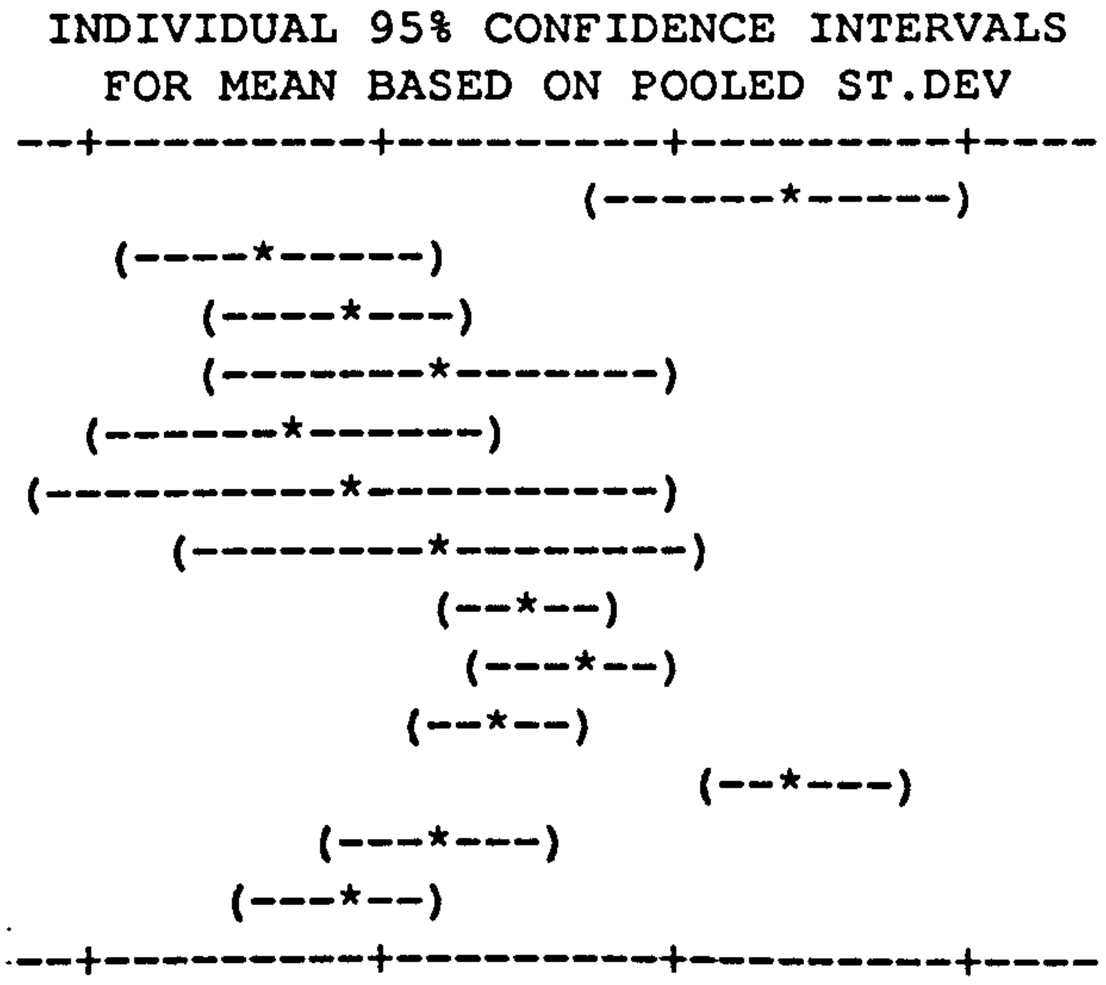
Nasion-Prosthion Height (NPH)

MALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	12	1067.6	89.0	5.75
WITHIN-GROUP	318	4920.4	15.5	
TOTAL	330	5988.0		

GROUP	N	MEAN	ST.DEV
Sindos	12	71.250	5.137
Pieria	15	65.267	4.317
Lerna	23	66.087	2.983
Athens-M	8	67.250	3.536
Athens-G	10	65.400	3.340
Fortetsa	4	66.250	2.754
Pyrgos	6	67.167	2.639
Giza	55	68.418	2.929
Kerma	43	68.814	4.188
Naqada	50	67.900	4.604
Sedment	37	71.514	4.260
Badari	34	67.147	3.986
Teita	34	66.000	3.939

POOLED ST.DEV = 3.934

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV

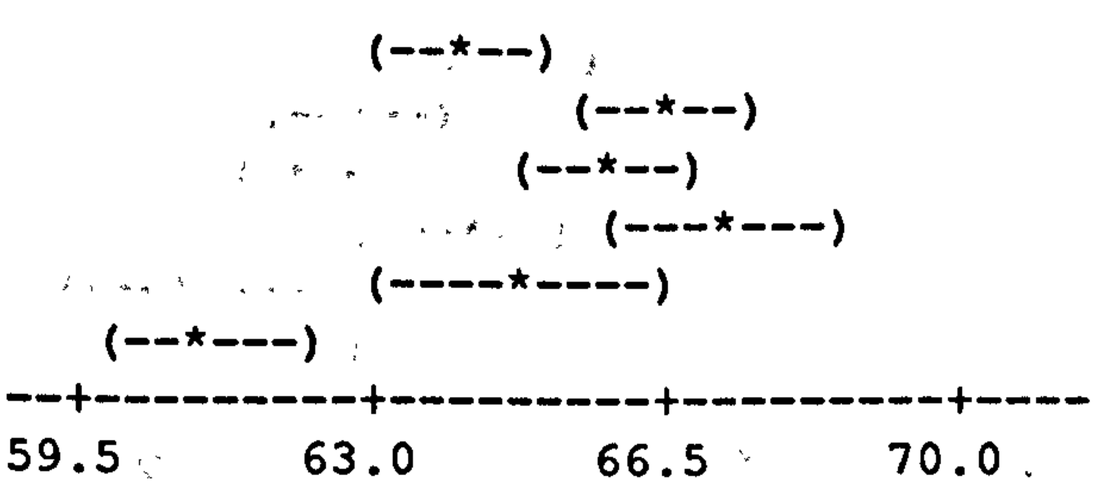


FEMALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	9	1131.4	125.7	8.97
WITHIN-GROUP	260	3642.1	14.0	
TOTAL	269	4773.5		

GROUP	N	MEAN	ST.DEV
Sindos	4	66.500	1.291
Pieria	6	64.500	3.619
Lerna	9	61.333	3.041
Athens-M	12	63.000	4.492
Athens-G			
Fortetsa			
Pyrgos			
Giza	52	64.135	3.326
Kerma	41	66.537	3.107
Naqada	51	65.667	3.548
Sedment	28	67.143	4.143
Badari	20	64.750	4.447
Teita	47	61.064	4.316

POOLED ST.DEV = 3.743

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV



APPENDIX 1

TABLE A1.2.6.

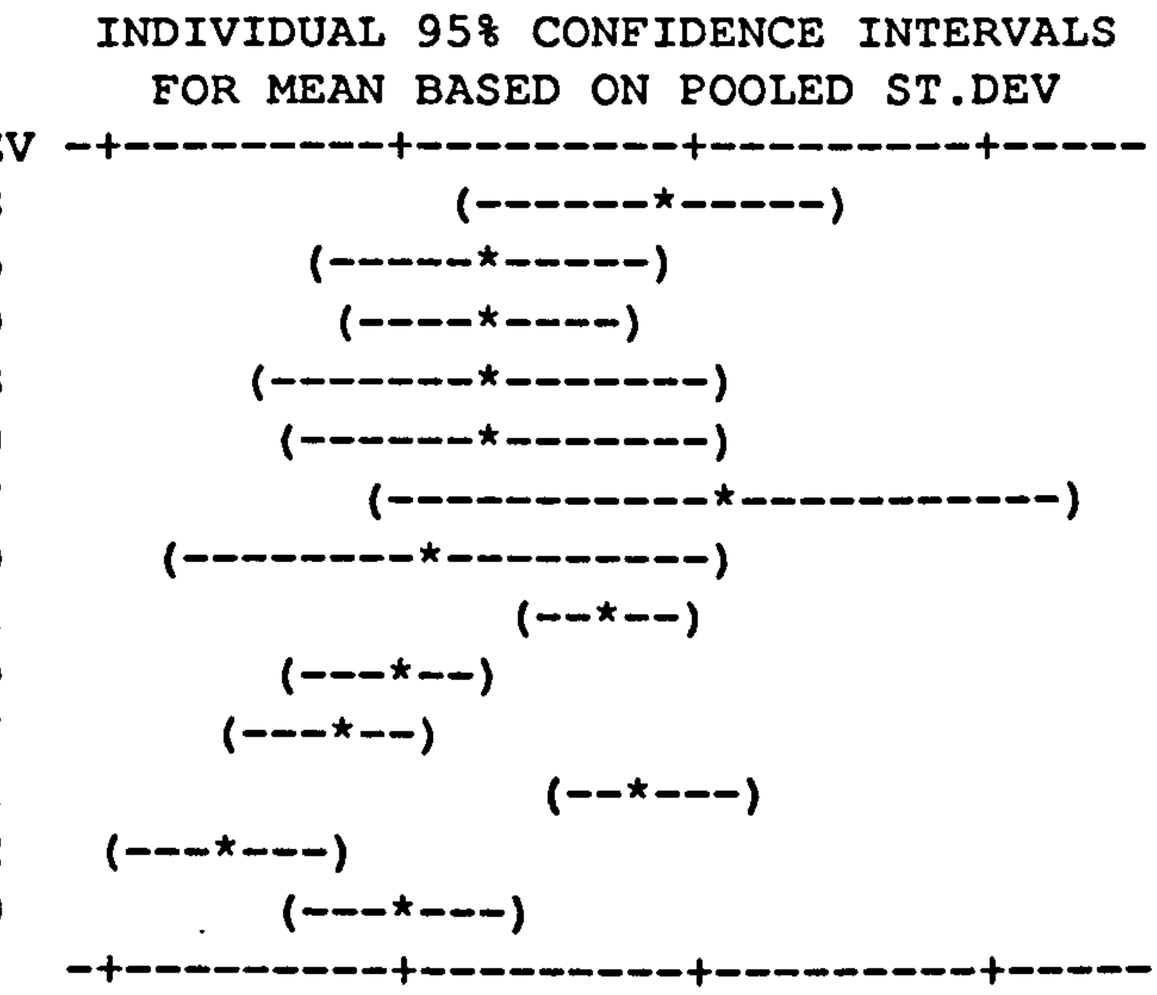
ANALYSIS OF VARIANCE OF CRANIAL MEASUREMENTS IN 13 GROUPS.

Nasal Height (NLH)

MALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	12	464.31	38.69	4.44
WITHIN-GROUP	318	2768.40	8.71	
TOTAL	330	3232.71		

GROUP	N	MEAN	ST.DEV
Sindos	13	52.231	3.723
Pieria	15	50.733	3.535
Lerna	22	50.682	2.679
Athens-M	8	50.750	2.053
Athens-G	10	50.800	2.300
Fortetsa	4	52.750	0.957
Pyrgos	6	50.333	3.559
Giza	55	51.727	2.704
Kerma	43	49.884	3.179
Naqada	50	49.400	3.017
Sedment	37	52.081	3.174
Badari	34	48.441	2.732
Teita	34	50.088	2.800

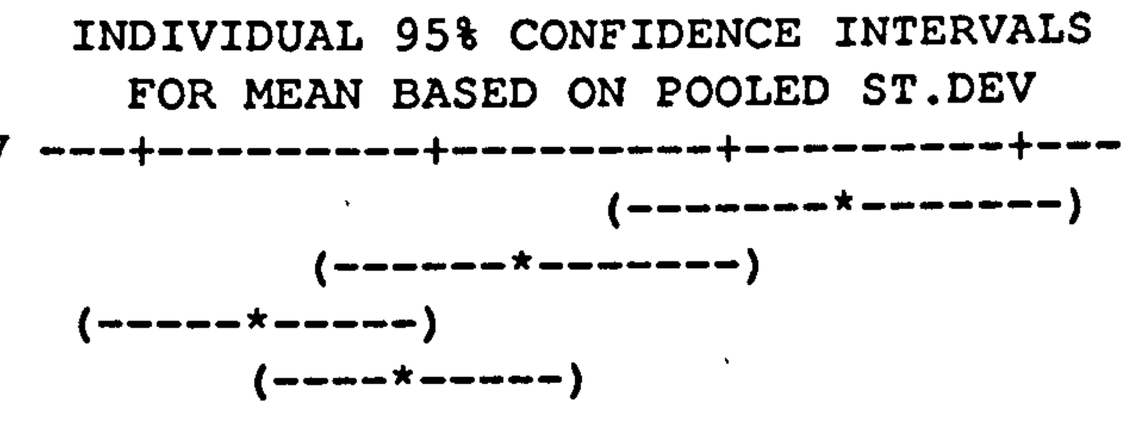
POOLED ST.DEV = 2.951



FEMALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	9	418.27	46.47	5.85
WITHIN-GROUP	261	2075.07	7.95	
TOTAL	270	2493.34		

GROUP	N	MEAN	ST.DEV
Sindos	5	52.200	4.382
Pieria	6	49.000	1.789
Lerna	9	46.111	3.180
Athens-M	12	47.833	4.086
Athens-G			
Fortetsa			
Pyrgos			
Giza	52	48.981	2.288
Kerma	41	47.390	2.397
Naqada	51	46.922	2.777
Sedment	28	48.500	2.603
Badari	20	45.650	2.852
Teita	47	46.489	3.289

POOLED ST.DEV = 2.820



APPENDIX 1

TABLE A1.2.7.

ANALYSIS OF VARIANCE OF CRANIAL MEASUREMENTS IN 13 GROUPS.

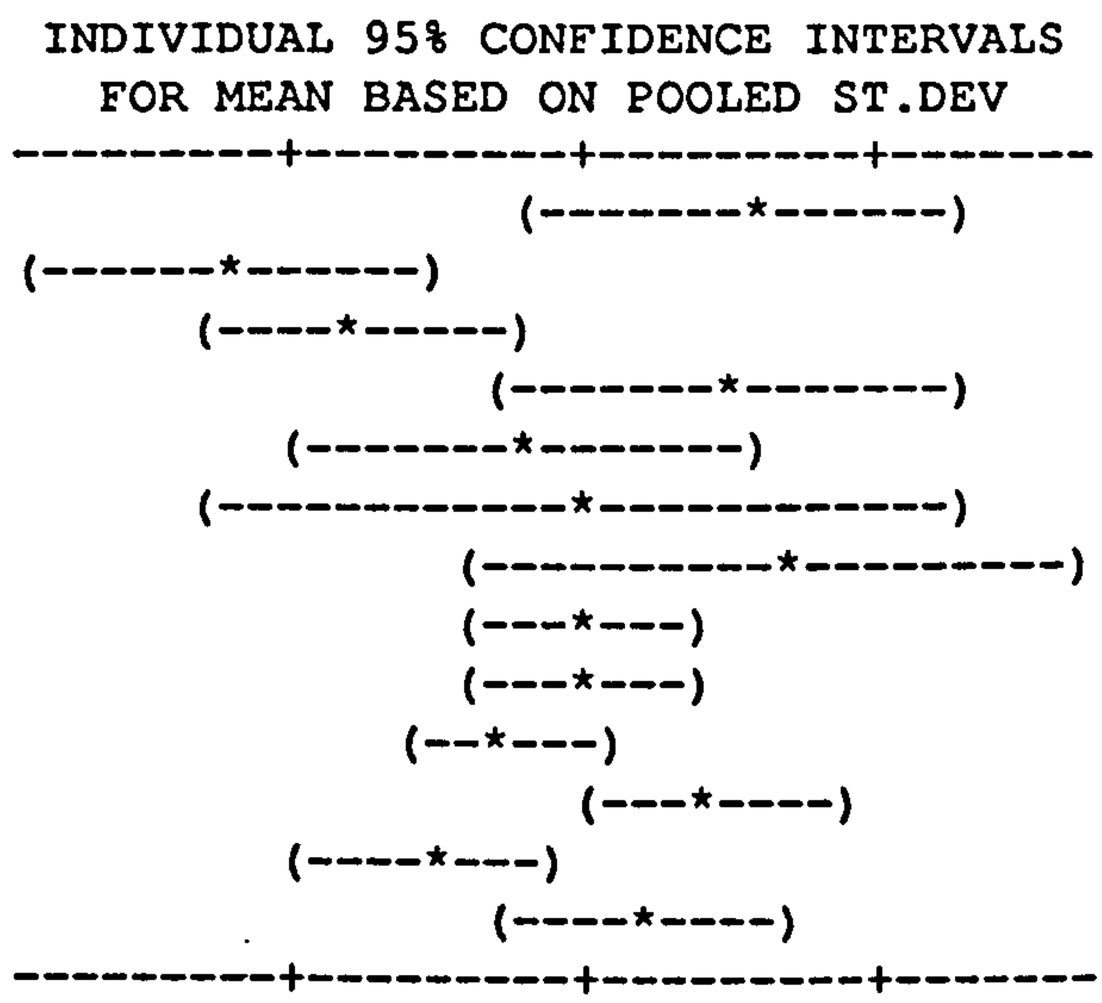
Orbital Height (OBB)

MALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	12	141.35	11.78	2.80
WITHIN-GROUP	322	1354.48	4.21	
TOTAL	334	1495.83		

GROUP	N	MEAN	ST.DEV
Sindos	12	33.833	2.480
Pieria	15	31.200	1.699
Lerna	23	31.826	2.289
Athens-M	11	33.727	1.954
Athens-G	12	32.667	1.155
Fortetsa	4	33.000	1.414
Pyrgos	7	34.000	1.732
Giza	55	32.982	2.032
Kerma	43	32.977	2.252
Naqada	50	32.620	2.267
Sedment	36	33.611	1.917
Badari	33	32.182	1.976
Teita	34	33.294	1.851

POOLED ST.DEV = 2.051

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV

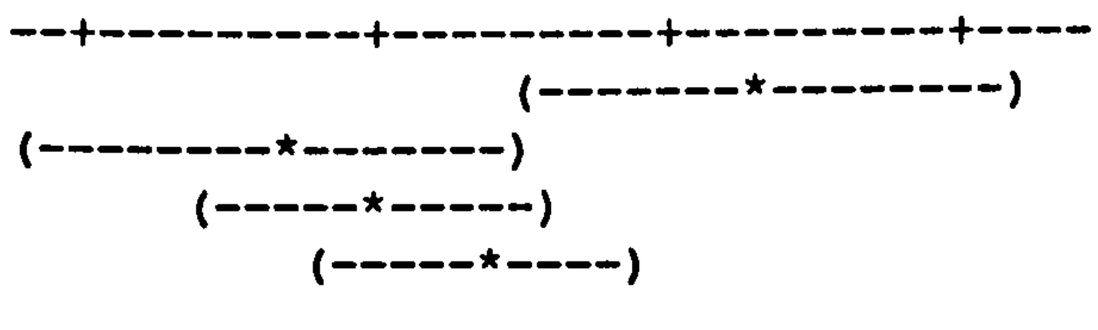


FEMALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	9	77.00	8.56	2.04
WITHIN-GROUP	263	1104.25	4.20	
TOTAL	272	1181.25		

GROUP	N	MEAN	ST.DEV
Sindos	6	34.667	1.366
Pieria	6	31.333	1.506
Lerna	11	32.000	3.098
Athens-M	13	32.769	2.862
Athens-G			
Fortetsa			
Pyrgos			
Giza	52	32.750	1.736
Kerma	41	32.683	2.138
Naqada	51	32.314	2.140
Sedment	28	32.714	1.960
Badari	18	31.333	1.940
Teita	47	32.149	1.841

POOLED ST.DEV = 2.049

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV



APPENDIX 1

TABLE A1.2.8.

ANALYSIS OF VARIANCE OF CRANIAL MEASUREMENTS IN 13 GROUPS.

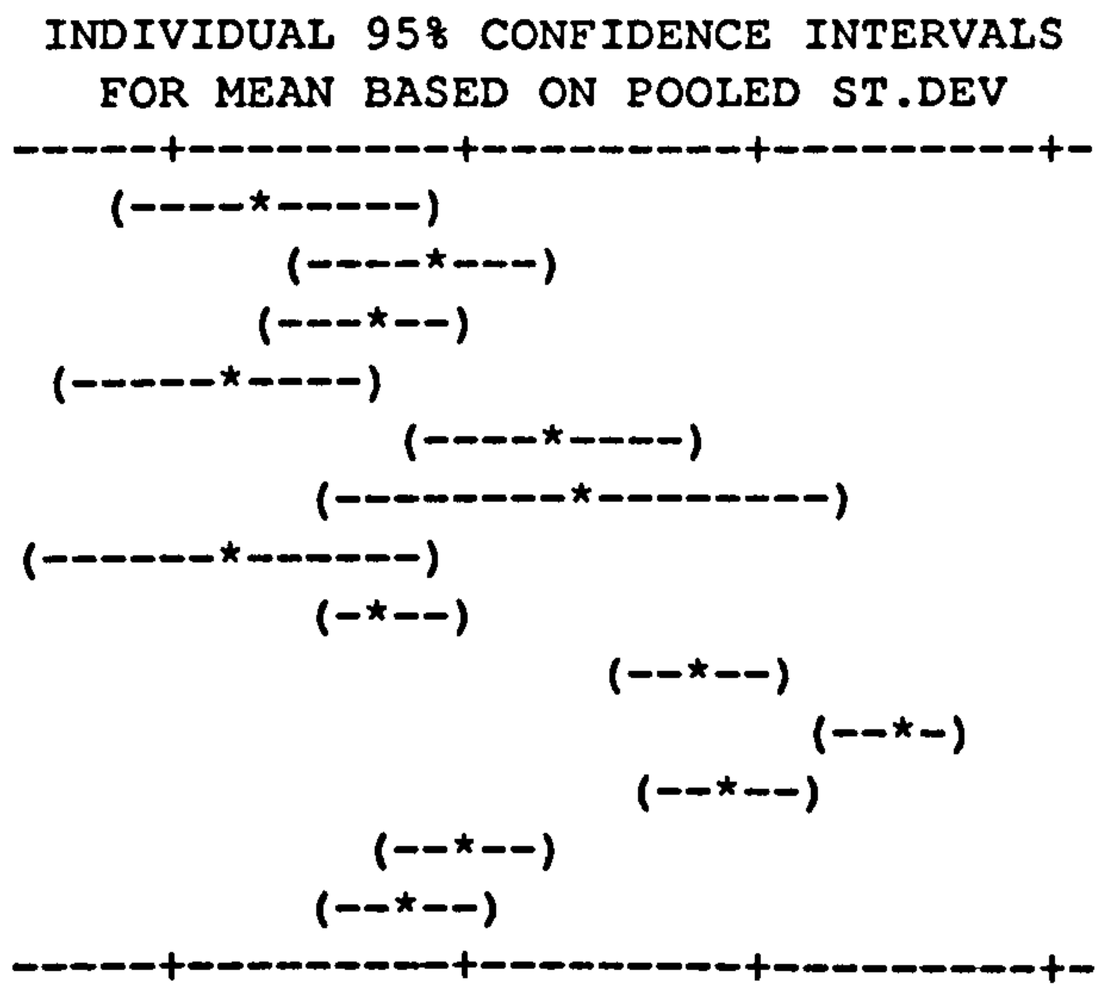
Orbital Breadth (OBB)

MALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	12	679.66	56.64	16.23
WITHIN-GROUP	325	1134.34	3.49	
TOTAL	337	1814.00		

GROUP	N	MEAN	ST.DEV
Sindos	13	38.692	1.797
Pieria	15	39.733	1.534
Lerna	25	39.320	1.282
Athens-M	11	38.364	2.063
Athens-G	12	40.583	1.881
Fortetsa	4	40.750	1.500
Pyrgos	7	38.429	2.507
Giza	55	39.418	1.750
Kerma	43	41.628	1.662
Naqada	50	42.940	2.342
Sedment	35	41.857	2.290
Badari	34	40.029	1.660
Teita	34	39.647	1.535

POOLED ST.DEV = 1.868

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV

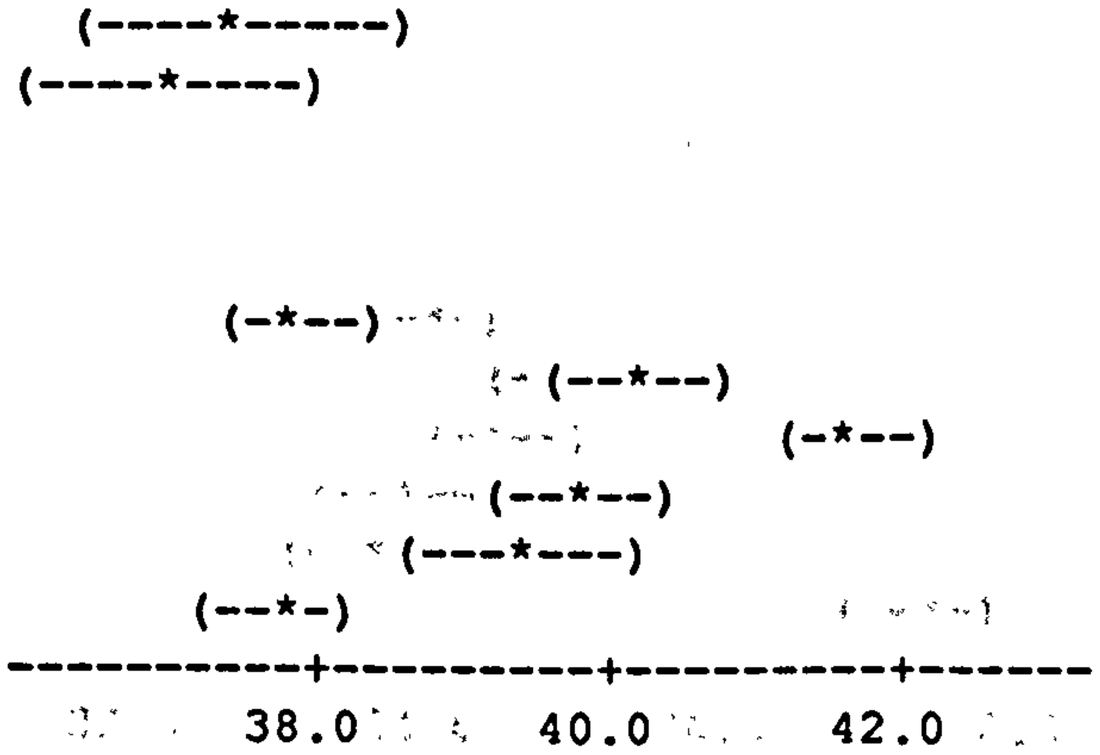


FEMALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	9	648.72	72.08	22.04
WITHIN-GROUP	262	856.81	3.27	
TOTAL	271	1505.53		

GROUP	N	MEAN	ST.DEV
Sindos	5	39.400	1.817
Pieria	6	38.167	1.169
Lerna	11	37.455	1.864
Athens-M	13	37.077	1.553
Athens-G			
Fortetsa			
Pyrgos			
Giza	52	37.827	1.593
Kerma	41	40.195	1.750
Naqada	51	41.627	2.254
Sedment	28	39.821	2.161
Badari	18	39.389	1.501
Teita	47	37.745	1.496

POOLED ST.DEV = 1.808

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV



APPENDIX 1

TABLE A1.2.9.

ANALYSIS OF VARIANCE OF CRANIAL MEASUREMENTS IN 13 GROUPS.

Nasal Breadth (NLB)

MALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	12	407.44	33.95	10.28
WITHIN-GROUP	313	1034.29	3.30	
TOTAL	325	1441.73		

GROUP	N	MEAN	ST.DEV	INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV
Sindos	12	25.083	1.676	(---*--)
Pieria	15	24.333	2.257	(--*--)
Lerna	21	25.000	2.098	(-*--)
Athens-M	8	23.625	1.061	(---*---)
Athens-G	8	23.625	1.408	(---*---)
Fortetsa	4	28.250	1.708	(-----*-----)
Pyrgos	4	22.500	2.380	(-----*-----)
Giza	55	24.818	1.733	(-*)
Kerma	43	25.837	1.825	(-*-)
Naqada	50	25.300	1.854	(*-)
Sedment	38	24.579	1.884	(-*-)
Badari	34	25.000	1.633	(-*-)
Teita	34	27.912	1.798	(-*-)
				-+---------+---------+---------+-----
POOLED ST.DEV =		1.818		21.0 24.0 27.0 30.0

FEMALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN-GROUP	9	512.24	56.92	19.65
WITHIN-GROUP	262	758.73	2.90	
TOTAL	271	1270.97		

GROUP	N	MEAN	ST.DEV	INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV
Sindos	5	23.200	1.789	(------*------)
Pieria	6	24.500	1.049	(------*-----)
Lerna	11	22.636	1.206	(----*----)
Athens-M	11	22.364	2.461	(----*----)
Athens-G				
Fortetsa				
Pyrgos				
Giza	52	24.019	1.578	(-*-)
Kerma	41	24.927	1.903	(--*-)
Naqada	51	24.471	1.713	(-*--)
Sedment	28	23.821	1.701	(--*--)
Badari	20	23.650	1.089	(--*---)
Teita	47	27.319	1.783	(--*-)
				----+---------+---------+---------+--
POOLED ST.DEV =		1.702		22.0 24.0 26.0 28.0

APPENDIX 1

TABLE A1.2.10

ANALYSIS OF VARIANCE OF CRANIAL MEASUREMENTS IN 13 GROUPS

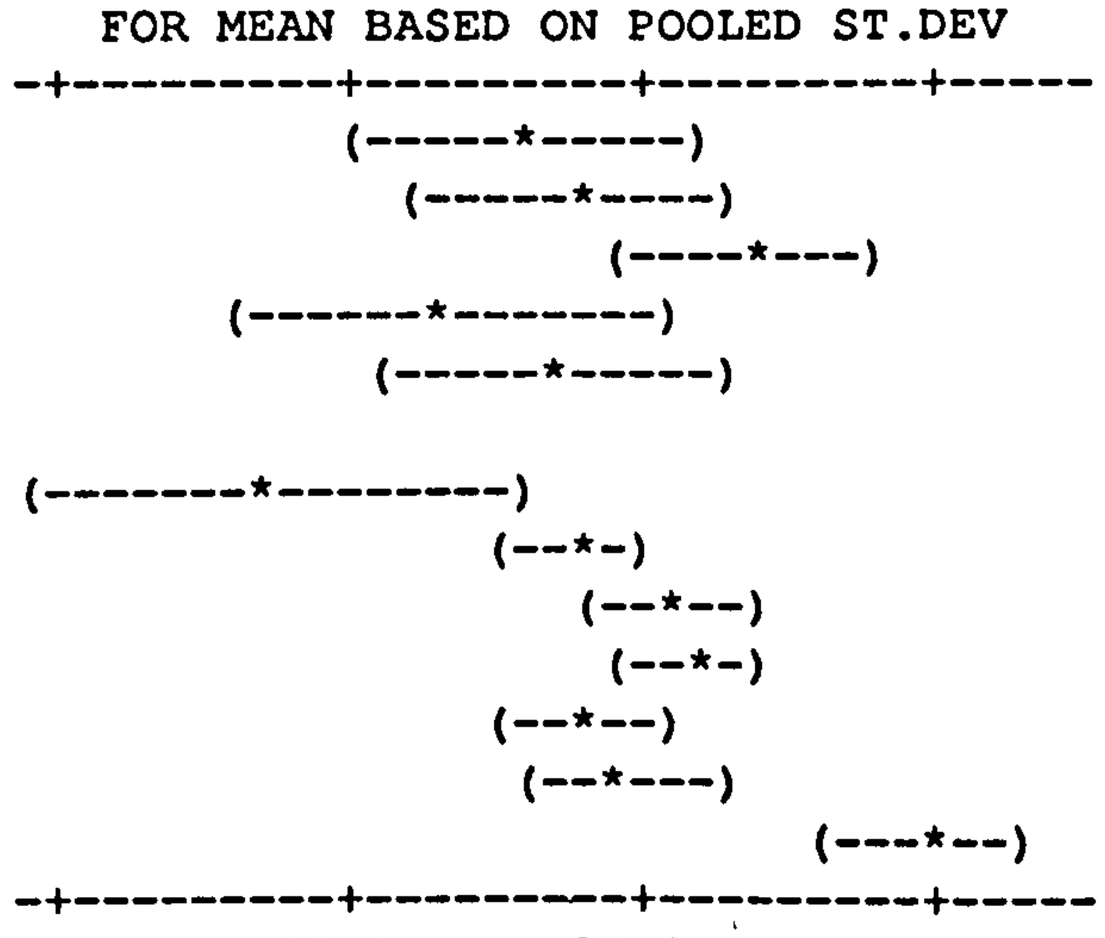
Bimaxillary Breadth (ZMB)

MALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN GROUP	11	1282.4	116.6	4.50
WITHIN GROUP	312	8081.0	25.9	
TOTAL	323	9363.4		

GROUP	N	MEAN	ST.DEV
Sindos	12	93.00	4.51
Pieria	14	93.86	6.19
Lerna	21	96.90	6.39
Athens-M	7	91.57	4.54
Athens-G	12	93.50	5.96
Fortetsa			
Pyrgos	6	88.67	2.80
Giza	55	93.87	4.35
Kerma	43	95.33	3.88
Naqada	50	95.82	5.91
Sedment	36	94.03	4.91
Badari	34	94.65	5.12
Teita	34	99.35	5.27

POOLED ST.DEV = 5.09

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV

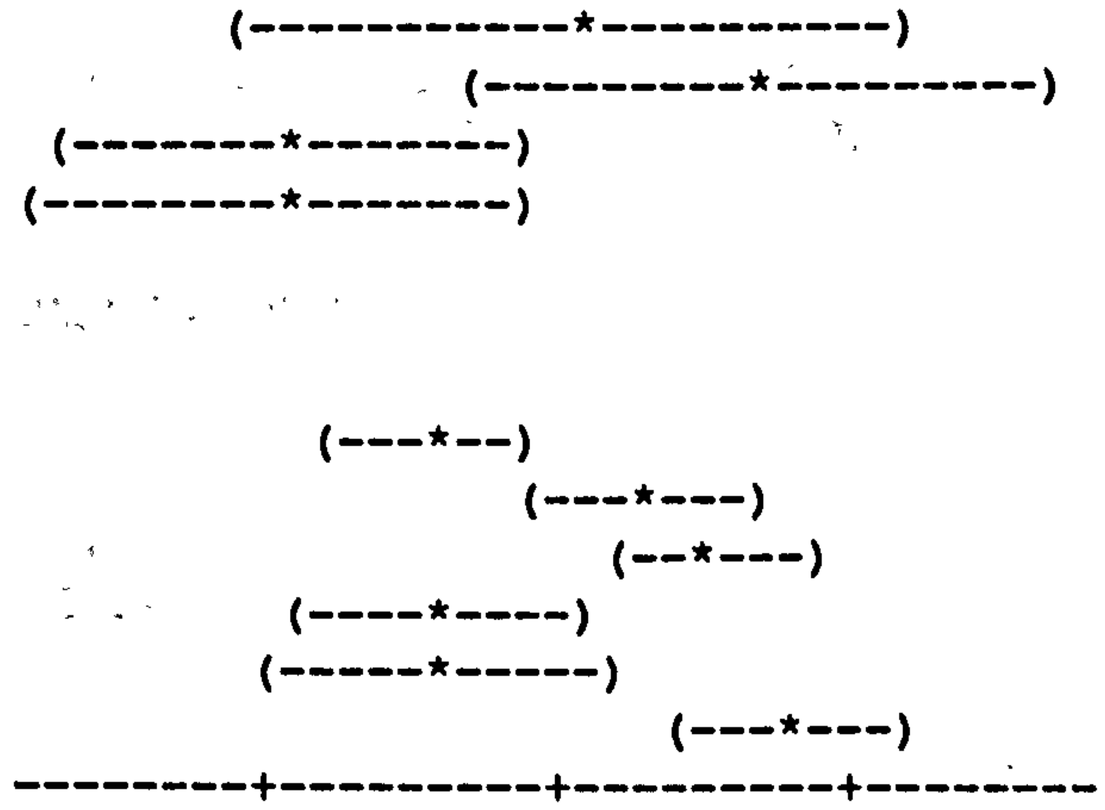


FEMALES	DF	SUM.SQ	MEAN.SQ	F-VALUE
BETWEEN GROUP	9	1016.0	112.9	5.63
WITHIN GROUP	256	5131.5	20.0	
TOTAL	265	6147.5		

GROUP	N	MEAN	ST.DEV
Sindos	5	91.200	3.564
Pieria	6	93.500	3.674
Lernaa	10	87.900	4.771
Athens-M	9	87.778	5.069
Athens-G			
Fortetsa			
Pyrgos			
Giza	52	89.481	4.775
Kerma	41	92.000	4.674
Naqada	51	92.882	4.302
Sedment	27	89.481	4.004
Badari	18	89.556	3.869
Teita	47	93.809	4.590

POOLED ST.DEV = 4.477

INDIVIDUAL 95% CONFIDENCE INTERVALS FOR MEAN BASED ON POOLED ST.DEV



APPENDIX 1

TABLE A1.3

MAHALANOBIS DISTANCES FOR 6 AFRICAN POPULATIONS (MALES)

AND THEIR SIGNIFICANCE (F-VALUES)

9 variables used: GOL, BNL, XCB, ZYB, NPH, NLH, OBH, NLB, ZMB.

Mahalanobis Distances (D)

Kerma (43)	1.7037				
Naqada (50)	1.7546	0.9695			
Sedment (27)	1.6485	1.7214	1.9954		
Badari (32)	2.4770	1.4259	0.9179	2.5028	
Teita (34)	3.2622	2.3754	2.7097	3.6708	2.8481
	Giza (55)	Kerma .(43)	Naqada (50)	Sedment (27)	Badari (32)

(Sample size shown in parentheses beneath each site-name)

Significance of the distance (F-values).

Kerma (43)	7.518**				
Naqada (50)	8.654**	2.332*			
Sedment (27)	5.282**	5.275**	7.493**		
Badari (32)	13.321**	4.004**	1.764	9.845**	
Kenya (34)	23.998**	11.498**	15.949**	21.765**	14.352**
	Giza (55)	Kerma .(43)	Naqada (50)	Sedment (27)	Badari (32)

(Degrees of freedom, num. 9, denom. 227)

F value for testing the overall equality of the group means.

F value:	8.786**	
Degrees of freedom:	numerator	45
	denominator	1019

* - $p < 0.05$
** - $p < 0.01$

APPENDIX 1

TABLE A1.4

MAHALANOBIS DISTANCES FOR 6 AFRICAN POPULATIONS (FEMALES)

AND THEIR SIGNIFICANCE (F-VALUES)

9 variables used: GOL, BNL, XCB, ZYB, NPH, NLH, OBH, NLB, ZMB.

Mahalanobis Distances (D)

Kerma (41)	2.2040				
Naqada (51)	2.2071	0.8793			
Sedment (24)	1.7268	1.8652	1.9750		
Badari (12)	2.1031	1.3177	1.2233	2.0723	
Teita (47)	3.9177	3.1860	3.6224	4.4266	3.7885
	Giza (52)	Kerma (41)	Naqada (51)	Sedment (24)	Badari (12)

(Sample size shown in parentheses beneath each site-name)

Significance of the distance (F-values).

Kerma (41)	11.925 **				
Naqada (51)	13.432**	1.882			
Sedment (24)	5.244**	5.640**	6.817**		
Badari (12)	4.618**	1.726	1.557	0.679	
Kenya (47)	40.577**	23.803**	34.370**	3.338**	14.693**
	Giza (52)	Kerma (41)	Naqada (51)	Sedment (24)	Badari (12)

(Degrees of freedom, num. 9, denom. 213)

F value for testing the overall equality of the group means.

F value: 11.621**

Degrees of freedom: numerator 45
denominator 956

* - $p < 0.05$
** - $p < 0.01$

TABLE A1.5.

MAHALANOBIS DISTANCES FOR 11 GREEK & AFRICAN POPULATIONS (MALES)

AND THEIR SIGNIFICANCE (F-VALUES)

5 variables used: GOL, XCB, NPH, OBH, NLB

Mahalanobis Distances (D)

(Sample size shown in parentheses beneath each site-name)

	Sindos (7)	Pieria (14)	Lerna (16)	Athens-M (8)	Athens-G (7)	Giza (55)	Kerma (43)	Naqada (50)	Sedment (35)	Badari (33)
Pieria (14)	1.7028									
Lerna (16)	1.8535	1.3537								
Athens-M (8)	1.7295	2.0498	1.5120							
Athens-G (7)	1.7220	1.1740	1.1523	1.0680						
Giza (55)	1.2600	1.4144	1.0351	1.5498	1.1986					
Kerma (43)	2.0746	2.1787	1.7703	2.5387	2.1806	1.1137				
Naqada (50)	2.2509	2.1560	1.6515	2.4246	2.0174	1.1043	0.4646			
Sedment (35)	1.4623	2.0820	2.2834	2.5900	2.2346	1.3220	1.3961	1.5998		
Badari (33)	2.9731	2.6956	2.2643	3.0237	2.5437	1.8212	1.0986	0.7759	2.0949	
Teita (34)	3.7365	3.6813	3.0563	3.8657	3.6284	2.8303	1.9215	1.9993	3.2174	1.9537

TABLE A1.5 CONTINUED.

MAHALANOBIS DISTANCES AND THEIR SIGNIFICANCE (F-VALUES).

Significance of the distance (F-values).

(Degrees of freedom, num. 5, denom. 287)

* - $p < 0.05$
** - $p < 0.01$

Pieria (14)	2.669*									
Lerna (16)	3.300*	2.699*								
Athens-M (8)	2.203	4.219**	2.405							
Athens-G (7)	2.047	1.269	1.275	0.840						
Giza (55)	1.945	4.404**	2.619	3.309*	1.760					
Kerma (43)	5.110**	9.888**	7.208**	8.575**	5.646**	5.904**				
Naqada (50)	6.137**	10.029**	6.521**	7.997**	4.929**	6.300**	0.984			
Sedment (35)	2.460	8.550**	11.293**	8.616**	5.746**	7.373**	7.418**	10.394**		
Badari (33)	10.069**	14.089**	10.897**	11.613**	7.371**	13.494**	4.445**	2.361	14.704**	
Teita (34)	15.986**	26.509**	20.047**	19.090**	15.075**	33.200**	13.827**	15.956**	35.216**	12.608**
	Sindos (7)	Pieria (14)	Lerna (16)	Athens-M (8)	Athens-G (7)	Giza (55)	Kerma (43)	Naqada (50)	Sedment (35)	Badari (33)

F value for testing the overall equality of the group means.

F value: 8.333** Degrees of freedom: numerator 50 denominator 1312

TABLE A1.6.

MAHALANOBIS DISTANCES FOR 11 GREEK & AFRICAN POPULATIONS (POOLED SEXES)

AND THEIR SIGNIFICANCE (F-VALUES)

5 variables used: GOL, XCB, NPH, OBH, NLB

Mahalanobis Distances (D)

(Sample size shown in parentheses beneath each site-name)

Pieria (20)	1.6089									
(Lerna (23)	1.7845	1.2325								
Athens-M (17)	1.8394	1.9901	1.1400							
Athens-G (8)	1.6283	1.4917	0.8762	0.7464						
Giza (107)	1.4867	1.2664	0.9068	1.3897	1.4064					
Kerma (84)	2.4398	2.2334	1.8559	2.3882	2.5546	1.2420				
Naqada (101)	2.3902	2.0956	1.5729	2.0982	2.2768	1.0752	0.4123			
Sedment (62)	1.7018	1.8304	2.0529	2.4243	2.4324	1.2797	1.3773	1.4570		
Badari (49)	2.8576	2.5052	1.8812	2.3624	2.5829	1.5626	0.8261	0.5711	1.8532	
Teita (81)	4.3391	3.8332	3.3672	3.8638	4.1009	3.0459	2.2297	2.3605	3.4801	2.3736
	Sindos (9)	Pieria (20)	Lerna (23)	Athens-M (17)	Athens-G (8)	Giza (107)	Kerma (84)	Naqada (101)	Sedment (62)	Badari (49)

TABLE A1.6 CONTINUED.

MAHALANOBIS DISTANCES AND THEIR SIGNIFICANCE (F-VALUES).

Significance of the distances (F-values).

Pieria (20)	3.190*									
Lerna (23)	4.090**	3.226*								
Athens-M (17)	3.953**	7.226**	2.522							
Athens-G (8)	2.230	2.524	0.905	0.602						
Giza (107)	3.643**	5.366**	3.091*	5.625**	2.923*					
Kerma (84)	9.608**	15.998**	12.348**	16.011**	9.465**	14.413**				
Naqada (101)	9.373**	14.555**	9.202**	12.719**	7.630**	11.926**	1.548			
Sedment (62)	4.519**	10.059**	14.038**	15.568**	8.324**	12.763**	13.435**	16.192**		
Badari (49)	12.327**	17.698**	10.998**	13.985**	9.109**	16.294**	4.194**	2.136	18.663**	
Teita (81)	30.279**	46.793**	40.325**	41.648**	24.311**	84.920**	40.705**	49.729**	84.447**	34.152**
	Sindos (9)	Pieria (20)	Lerna (23)	Athens-M (17)	Athens-G (8)	Giza (107)	Kerma (84)	Naqada (101)	Sedment (62)	Badari (49)

(Degrees of freedom, num. 5, denom. 546)

* - $p < 0.05$

** - $p < 0.01$

F value for testing the overall equality of the group means.

F value: 16.054** Degrees of freedom: numerator 50 denominator 2494

TABLE A1.7

MAHALANOBIS DISTANCE FOR 5 GREEK POPULATIONS (MALES)

AND THEIR SIGNIFICANCE (F-VALUES)

5 variables used: GOL, XCB, NPH, OBH, NLB

Mahalanobis Distances (D)

Pieria (14)	1.8168			
Lerna (16)	1.8338	1.2641		
Athens-M (8)	1.5983	1.7717	1.3990	
Athens-G (7)	1.8047	0.9553	1.1685	1.0060
	Sindos (7)	Pieria (14)	Lerna (16)	Athens-M (8)

(Sample size shown in parentheses beneath each site-name)

Significance of the distance (F-values).

Pieria (14)	2.819			
Lerna (16)	2.996*	2.183		
Athens-M (8)	1.745	2.934*	1.910	
Athens-G (7)	2.086	0.779	1.217	0.691
	Sindos (7)	Pieria (14)	Lerna (16)	Athens-M (8)

(Degrees of freedom, num. 5, denom. 43)

F value for testing the overall equality of the group means.

F value:	1.962*	
Degrees of freedom:	numerator	20
	denominator	144

* - $p < 0.05$

TABLE A1.8

MAHALANOBIS DISTANCE FOR 5 GREEK POPULATIONS (POOLED SEXES) AND THEIR SIGNIFICANCE (F-VALUES)

5 variables used: GOL, XCB, NPH, OBH, NLB

Mahalanobis Distances (D)

Pieria (20)	1.5234			(Sample size shown in parentheses beneath each site-name)
Lerna (23)	1.6901	0.9965		
Athens-M (17)	1.7122	1.6632	1.0146	
Athens-G (8)	1.5860	1.2962	0.8501	0.6174
	Sindos (9)	Pieria (20)	Lerna (23)	Athens-M (17)

Significance of the distance (F-values).

Pieria (20)	2.721			(Degrees of freedom, num. 5, denom. 68)
Lerna (23)	3.490*	2.006		
Athens-M (17)	3.259*	4.801*	1.901	
Athens-G (8)	2.012	1.813	0.810	0.392
	Sindos (9)	Pieria (20)	Lerna (23)	Athens-M (17)

F value for testing the overall equality of the group means.

F value: 2.305*

Degrees of freedom: numerator 20
denominator 226

* - $p < 0.05$

APPENDIX 2

BASIC STATISTICS - NON-METRIC TRAITS.

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Trait frequencies for 6 African groups: Right side only

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Trait frequencies for 13 Greek and African groups (pooled sexes) : Right side only

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APPENDIX 2

TABLE A2.1.1.

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - males.

LEFT SIDE ONLY.

	GIZA		KERMA		NAQADA	
	trait present / no.	freq.	trait present / no.	freq.	trait present / no.	freq.
1. HiNuLin	27 / 55	0.491	21 / 43	0.488	31 / 49	0.633
2. OsAtLam *	12 / 55	0.218	2 / 43	0.047	4 / 50	0.080
3. OsLambd	20 / 55	0.364	15 / 43	0.349	17 / 50	0.340
4. FPariet	23 / 55	0.418	17 / 43	0.395	20 / 49	0.408
5. OsBreg *	0 / 55	0.000	0 / 43	0.000	1 / 49	0.020
6. SuMetop *	0 / 55	0.000	0 / 43	0.000	1 / 50	0.020
7. OsCoron	0 / 55	0.000	0 / 43	0.000	2 / 50	0.040
8. OsPter	6 / 55	0.109	1 / 42	0.024	6 / 48	0.125
9. FrTemAr	0 / 55	0.000	4 / 42	0.095	1 / 49	0.020
10. OsPaNot	2 / 55	0.036	2 / 42	0.048	3 / 50	0.060
11. OsAster	2 / 55	0.036	1 / 43	0.023	3 / 50	0.060
12. TorAud	1 / 55	0.018	0 / 43	0.000	2 / 50	0.040
13. FHusch	3 / 55	0.055	4 / 42	0.095	6 / 50	0.120
14. FMasEx	16 / 35	0.457	8 / 18	0.444	14 / 30	0.467
15. FMasAb	20 / 55	0.364	25 / 43	0.581	20 / 50	0.400
16. CanConP	34 / 55	0.618	24 / 42	0.571	28 / 49	0.571
17. BifaCon	1 / 54	0.019	0 / 42	0.000	0 / 46	0.000
18. TubConA	11 / 55	0.200	4 / 43	0.093	11 / 49	0.224
19. BrCanHy	13 / 55	0.236	9 / 43	0.209	8 / 49	0.163
20. FOvSpOp	0 / 55	0.000	1 / 43	0.023	1 / 50	0.020
21. FSpOp	6 / 55	0.109	4 / 42	0.095	8 / 50	0.160
22. FLPalAc	45 / 55	0.818	34 / 43	0.791	44 / 49	0.898
23. TorPal *	0 / 55	0.000	0 / 43	0.000	0 / 50	0.000
24. TorMax	0 / 55	0.000	0 / 43	0.000	0 / 50	0.000
25. FZyFAb	14 / 55	0.255	11 / 42	0.262	8 / 49	0.163
26. FSupOrb	12 / 55	0.218	7 / 42	0.167	8 / 50	0.160
27. FNotFr	4 / 55	0.073	5 / 42	0.119	5 / 50	0.100
28. FAEthEx	17 / 54	0.315	11 / 36	0.306	18 / 42	0.429
29. FPEthAb	1 / 53	0.019	1 / 38	0.026	2 / 41	0.049
30. FIOrbAc	8 / 55	0.145	3 / 42	0.071	5 / 49	0.102

* - Midline trait

APPENDIX 2

TABLE A2.1.1 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - males.

LEFT SIDE ONLY.

	GIZA			KERMA			NAQADA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
31. OsInca *	2	/ 55	0.036	3	/ 43	0.070	2	/ 50	0.040
32. SulOrb	10	/ 55	0.182	7	/ 42	0.167	18	/ 49	0.367
33. NasSill	44	/ 55	0.800	32	/ 43	0.744	43	/ 48	0.896
34. FNasal	45	/ 54	0.833	34	/ 34	1.000	41	/ 43	0.953
35. CribOrb	10	/ 55	0.182	1	/ 43	0.023	3	/ 50	0.060
36. SpurTro	1	/ 55	0.018	2	/ 41	0.049	5	/ 49	0.102
37. FosTro	17	/ 55	0.309	10	/ 41	0.244	23	/ 49	0.469
38. GrFront	10	/ 55	0.182	9	/ 43	0.209	17	/ 49	0.347
39. OsSqPar	1	/ 55	0.018	1	/ 42	0.024	3	/ 48	0.063
40. SuJapTr	4	/ 55	0.073	1	/ 42	0.024	9	/ 46	0.196
41. ProcMar	1	/ 55	0.018	8	/ 43	0.186	1	/ 50	0.020
42. FZyTem	33	/ 55	0.600	31	/ 42	0.738	41	/ 50	0.820
43. FZyOrb	52	/ 55	0.945	39	/ 42	0.929	44	/ 50	0.880
44. OsOcMas	0	/ 55	0.000	1	/ 43	0.023	3	/ 50	0.060
45. CanConI	28	/ 55	0.509	16	/ 43	0.372	23	/ 49	0.469
46. TubConP	0	/ 55	0.000	0	/ 39	0.000	0	/ 47	0.000
47. BrJugF	6	/ 55	0.109	5	/ 43	0.116	10	/ 49	0.204
48. TubPhar *	21	/ 55	0.382	18	/ 43	0.419	19	/ 49	0.388
49. FosPhar *	9	/ 55	0.164	9	/ 43	0.209	6	/ 49	0.122
50. FOvOp	0	/ 55	0.000	1	/ 43	0.023	1	/ 50	0.020
51. FVesal	7	/ 55	0.127	8	/ 41	0.195	5	/ 50	0.100
52. BrPtBas	1	/ 55	0.018	3	/ 43	0.070	2	/ 49	0.041
53. BrPtSp	1	/ 55	0.018	0	/ 43	0.000	3	/ 45	0.067
54. BrSpBas	4	/ 55	0.073	2	/ 43	0.047	4	/ 48	0.083
55. SpinFOv	2	/ 55	0.036	5	/ 43	0.116	3	/ 50	0.060
56. FSpAc	2	/ 55	0.036	2	/ 43	0.047	3	/ 49	0.061
57. PerfPt	5	/ 53	0.094	0	/ 34	0.000	2	/ 37	0.054
58. SpurPt	36	/ 53	0.679	14	/ 31	0.452	19	/ 29	0.655
59. BrPal	7	/ 55	0.127	6	/ 43	0.140	10	/ 50	0.200
60. FZyFMu	18	/ 41	0.439	14	/ 31	0.452	12	/ 41	0.293

*** - Midline trait**

APPENDIX 2

TABLE A2.1.2.

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - males.

LEFT SIDE ONLY.

	SEDMENT			BADARI			TEITA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	23	/ 38	0.605	21	/ 36	0.583	15	/ 34	0.441
2. OsAtLam *	4	/ 39	0.103	3	/ 36	0.083	4	/ 34	0.118
3. OsLambd	14	/ 39	0.359	12	/ 36	0.333	10	/ 34	0.294
4. FPariet	13	/ 39	0.333	19	/ 36	0.528	13	/ 34	0.382
5. OsBreg *	0	/ 39	0.000	0	/ 36	0.000	0	/ 34	0.000
6. SuMetop *	2	/ 39	0.051	4	/ 35	0.114	1	/ 33	0.030
7. OsCoron	1	/ 38	0.026	1	/ 34	0.029	0	/ 34	0.000
8. OsPter	2	/ 38	0.053	5	/ 32	0.156	0	/ 33	0.000
9. FrTemAr	0	/ 38	0.000	0	/ 32	0.000	3	/ 34	0.088
10. OsPaNot	3	/ 39	0.077	7	/ 36	0.194	6	/ 34	0.176
11. OsAster	3	/ 39	0.077	2	/ 34	0.059	4	/ 34	0.118
12. TorAud	4	/ 38	0.105	1	/ 34	0.029	0	/ 34	0.000
13. FHusch	3	/ 37	0.081	5	/ 33	0.152	7	/ 33	0.212
14. FMasEx	9	/ 24	0.375	15	/ 24	0.625	9	/ 24	0.375
15. FMasAb	13	/ 37	0.351	10	/ 34	0.294	10	/ 34	0.294
16. CanConP	14	/ 36	0.389	18	/ 33	0.545	16	/ 32	0.500
17. BifaCon	0	/ 33	0.000	0	/ 31	0.000	0	/ 27	0.000
18. TubConA	9	/ 37	0.243	5	/ 32	0.156	1	/ 30	0.033
19. BrCanHy	7	/ 37	0.189	4	/ 33	0.121	3	/ 34	0.088
20. FOvSpOp	0	/ 38	0.000	0	/ 34	0.000	2	/ 34	0.059
21. FSpOp	6	/ 38	0.158	3	/ 32	0.094	5	/ 34	0.147
22. FLPalAc	31	/ 34	0.912	28	/ 31	0.903	29	/ 29	1.000
23. TorPal *	0	/ 36	0.000	0	/ 34	0.000	0	/ 33	0.000
24. TorMax	0	/ 38	0.000	0	/ 33	0.000	0	/ 34	0.000
25. FZyFAb	5	/ 38	0.132	6	/ 34	0.176	8	/ 31	0.258
26. FSupOrb	8	/ 39	0.205	7	/ 32	0.219	4	/ 34	0.118
27. FNotFr	6	/ 39	0.154	3	/ 34	0.088	4	/ 34	0.118
28. FAEthEx	8	/ 29	0.276	10	/ 25	0.400	14	/ 33	0.424
29. FPEthAb	0	/ 33	0.000	0	/ 25	0.000	0	/ 33	0.000
30. FIOrbAc	4	/ 33	0.121	2	/ 30	0.067	3	/ 32	0.094

* - Midline trait

APPENDIX 2

TABLE A2.1.2 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - males.

LEFT SIDE ONLY.

	SEDMENT			BADARI			TEITA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
31. OsInca *	0	/ 39	0.000	0	/ 36	0.000	1	/ 34	0.029
32. SulOrb	5	/ 33	0.152	10	/ 30	0.333	6	/ 31	0.194
33. NasSill	33	/ 38	0.868	26	/ 32	0.813	14	/ 34	0.412
34. FNasal	22	/ 31	0.710	21	/ 28	0.750	28	/ 30	0.933
35. CribOrb	2	/ 39	0.051	1	/ 35	0.029	2	/ 34	0.059
36. SpurTro	3	/ 33	0.091	2	/ 30	0.067	2	/ 34	0.059
37. FosTro	7	/ 33	0.212	5	/ 30	0.167	5	/ 34	0.147
38. GrFront	6	/ 39	0.154	9	/ 35	0.257	13	/ 34	0.382
39. OsSqPar	1	/ 37	0.027	1	/ 33	0.030	2	/ 34	0.059
40. SuJapTr	2	/ 32	0.063	4	/ 30	0.133	3	/ 30	0.100
41. ProcMar	3	/ 38	0.079	0	/ 34	0.000	2	/ 31	0.065
42. FZyTem	28	/ 38	0.737	23	/ 33	0.697	28	/ 33	0.848
43. FZyOrb	34	/ 38	0.895	31	/ 33	0.939	27	/ 33	0.818
44. OsOcMas	1	/ 37	0.027	3	/ 34	0.088	2	/ 34	0.059
45. CanConI	13	/ 34	0.382	17	/ 32	0.531	16	/ 33	0.485
46. TubConP	1	/ 35	0.029	1	/ 29	0.034	0	/ 34	0.000
47. BrJugF	7	/ 36	0.194	9	/ 31	0.290	3	/ 34	0.088
48. TubPhar *	13	/ 36	0.361	11	/ 33	0.333	8	/ 33	0.242
49. FosPhar *	6	/ 36	0.167	5	/ 33	0.152	3	/ 33	0.091
50. FOvOp	1	/ 38	0.026	0	/ 31	0.000	1	/ 34	0.029
51. FVesal	6	/ 38	0.158	5	/ 28	0.179	5	/ 31	0.161
52. BrPtBas	3	/ 38	0.079	2	/ 31	0.065	1	/ 31	0.032
53. BrPtSp	0	/ 36	0.000	1	/ 28	0.036	0	/ 31	0.000
54. BrSpBas	3	/ 38	0.079	3	/ 31	0.097	1	/ 34	0.029
55. SpinFOv	1	/ 37	0.027	1	/ 31	0.032	0	/ 34	0.000
56. FSpAc	2	/ 38	0.053	4	/ 31	0.129	2	/ 34	0.059
57. PerfPt	0	/ 28	0.000	2	/ 30	0.067	2	/ 25	0.080
58. SpurPt	12	/ 23	0.522	12	/ 16	0.750	7	/ 16	0.438
59. BrPal	5	/ 37	0.135	6	/ 31	0.194	6	/ 31	0.194
60. FZyFMu	14	/ 33	0.424	11	/ 28	0.393	4	/ 23	0.174

* - Midline trait

APPENDIX 2

TABLE A2.2.1.

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - females.

LEFT SIDE ONLY.

	GIZA			KERMA			NAQADA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	18	/ 52	0.346	22	/ 41	0.537	29	/ 51	0.569
2. OsAtLam *	7	/ 51	0.137	3	/ 41	0.073	6	/ 51	0.118
3. OsLambd	16	/ 51	0.314	13	/ 41	0.317	19	/ 51	0.373
4. FPariet	19	/ 52	0.365	22	/ 41	0.537	29	/ 51	0.569
5. OsBreg *	1	/ 52	0.019	1	/ 41	0.024	1	/ 51	0.020
6. SuMetop *	1	/ 52	0.019	2	/ 41	0.049	1	/ 50	0.020
7. OsCoron	1	/ 52	0.019	2	/ 41	0.049	1	/ 51	0.020
8. OsPter	3	/ 52	0.058	8	/ 40	0.200	10	/ 51	0.196
9. FrTemAr	1	/ 52	0.019	4	/ 40	0.100	0	/ 51	0.000
10. OsPaNot	5	/ 52	0.096	7	/ 40	0.175	5	/ 51	0.098
11. OsAster	2	/ 52	0.038	2	/ 41	0.049	3	/ 51	0.059
12. TorAud	0	/ 52	0.000	0	/ 41	0.000	0	/ 50	0.000
13. FHusch	16	/ 52	0.308	13	/ 40	0.325	7	/ 48	0.146
14. FMasEx	14	/ 32	0.438	9	/ 20	0.450	12	/ 29	0.414
15. FMasAb	20	/ 52	0.385	21	/ 41	0.512	22	/ 51	0.431
16. CanConP	29	/ 52	0.558	24	/ 37	0.649	36	/ 51	0.706
17. BifaCon	0	/ 52	0.000	0	/ 40	0.000	0	/ 50	0.000
18. TubConA	9	/ 52	0.173	7	/ 41	0.171	9	/ 51	0.176
19. BrCanHy	12	/ 52	0.231	7	/ 40	0.175	10	/ 51	0.196
20. FOvSpOp	0	/ 52	0.000	1	/ 41	0.024	0	/ 50	0.000
21. FSpOp	4	/ 52	0.077	6	/ 41	0.146	5	/ 49	0.102
22. FLPalAc	47	/ 52	0.904	32	/ 40	0.800	44	/ 49	0.898
23. TorPal *	0	/ 52	0.000	0	/ 39	0.000	0	/ 50	0.000
24. TorMax	0	/ 52	0.000	0	/ 41	0.000	0	/ 51	0.000
25. FZyFAb	12	/ 52	0.231	8	/ 41	0.195	9	/ 50	0.180
26. FSupOrb	8	/ 52	0.154	9	/ 41	0.220	10	/ 51	0.196
27. FNotFr	5	/ 52	0.096	4	/ 41	0.098	2	/ 50	0.040
28. FAEthEx	18	/ 50	0.360	14	/ 39	0.359	21	/ 48	0.438
29. FPEthAb	2	/ 51	0.039	0	/ 37	0.000	0	/ 48	0.000
30. FIOrbAc	6	/ 52	0.115	0	/ 41	0.000	4	/ 51	0.078

* - Midline trait

APPENDIX 2

TABLE A2.2.1 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - females.

LEFT SIDE ONLY.

	GIZA		KERMA		NAQADA	
	trait present / no.	freq.	trait present / no.	freq.	trait present / no.	freq.
31. OsInca *	1 / 52	0.019	0 / 41	0.000	0 / 51	0.000
32. SulOrb	18 / 52	0.346	13 / 41	0.317	26 / 50	0.520
33. NasSill	46 / 52	0.885	22 / 41	0.537	42 / 50	0.840
34. FNasal	44 / 51	0.863	29 / 33	0.879	33 / 38	0.868
35. CribOrb	6 / 52	0.115	4 / 41	0.098	4 / 51	0.078
36. SpurTro	10 / 52	0.192	6 / 41	0.146	7 / 50	0.140
37. FosTro	12 / 52	0.231	8 / 41	0.195	22 / 50	0.440
38. GrFront	12 / 52	0.231	14 / 41	0.341	11 / 51	0.216
39. OsSqPar	2 / 52	0.038	2 / 40	0.050	2 / 51	0.039
40. SuJapTr	4 / 52	0.077	0 / 41	0.000	2 / 48	0.042
41. ProcMar	2 / 52	0.038	2 / 41	0.049	4 / 49	0.082
42. FZyTem	37 / 51	0.725	29 / 41	0.707	35 / 50	0.700
43. FZyOrb	47 / 52	0.904	32 / 40	0.800	46 / 50	0.920
44. OsOcMas	0 / 52	0.000	5 / 40	0.125	4 / 51	0.078
45. CanConI	21 / 52	0.404	14 / 40	0.350	30 / 51	0.588
46. TubConP	0 / 52	0.000	0 / 38	0.000	0 / 50	0.000
47. BrJugF	9 / 52	0.173	7 / 40	0.175	9 / 51	0.176
48. TubPhar *	12 / 52	0.231	12 / 41	0.293	11 / 51	0.216
49. FosPhar *	10 / 52	0.192	11 / 41	0.268	13 / 51	0.255
50. FOvOp	1 / 52	0.019	1 / 40	0.025	0 / 51	0.000
51. FVesal	8 / 52	0.154	9 / 41	0.220	12 / 51	0.235
52. BrPtBas	2 / 52	0.038	0 / 41	0.000	0 / 50	0.000
53. BrPtSp	1 / 52	0.019	0 / 40	0.000	0 / 48	0.000
54. BrSpBas	7 / 52	0.135	3 / 41	0.073	4 / 50	0.080
55. SpinFOv	0 / 52	0.000	3 / 41	0.073	2 / 51	0.039
56. FSpAc	3 / 52	0.058	2 / 41	0.049	0 / 50	0.000
57. PerfPt	7 / 52	0.135	0 / 34	0.000	7 / 47	0.149
58. SpurPt	38 / 51	0.745	14 / 30	0.467	24 / 38	0.632
59. BrPal	12 / 52	0.231	11 / 41	0.268	12 / 51	0.235
60. FZyFMu	11 / 40	0.275	14 / 33	0.424	14 / 41	0.341

* - Midline trait

TABLE A2.2.2.

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - females.

LEFT SIDE ONLY.

	SEDMENT			BADARI			TEITA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	16	/ 29	0.552	9	/ 20	0.450	21	/ 47	0.447
2. OsAtLam *	6	/ 29	0.207	3	/ 21	0.143	8	/ 47	0.170
3. OsLambd	12	/ 29	0.414	9	/ 21	0.429	22	/ 47	0.468
4. FPariet	10	/ 29	0.345	7	/ 21	0.333	18	/ 47	0.383
5. OsBreg *	0	/ 29	0.000	0	/ 21	0.000	0	/ 47	0.000
6. SuMetop *	1	/ 28	0.036	0	/ 21	0.000	0	/ 47	0.000
7. OsCoron	2	/ 29	0.069	0	/ 21	0.000	0	/ 47	0.000
8. OsPter	9	/ 29	0.310	6	/ 20	0.300	4	/ 46	0.087
9. FrTemAr	0	/ 29	0.000	2	/ 20	0.100	3	/ 47	0.064
10. OsPaNot	2	/ 28	0.071	1	/ 21	0.048	8	/ 47	0.170
11. OsAster	2	/ 29	0.069	3	/ 21	0.143	4	/ 46	0.087
12. TorAud	2	/ 29	0.069	1	/ 22	0.045	0	/ 47	0.000
13. FHusch	8	/ 27	0.296	5	/ 22	0.227	20	/ 47	0.426
14. FMasEx	9	/ 15	0.600	9	/ 14	0.643	7	/ 24	0.292
15. FMasAb	13	/ 28	0.464	8	/ 22	0.364	22	/ 46	0.478
16. CanConP	15	/ 29	0.517	10	/ 20	0.500	31	/ 46	0.674
17. BifaCon	0	/ 28	0.000	2	/ 15	0.133	0	/ 37	0.000
18. TubConA	1	/ 29	0.034	0	/ 15	0.000	2	/ 46	0.043
19. BrCanHy	5	/ 29	0.172	6	/ 20	0.300	3	/ 46	0.065
20. FOvSpOp	1	/ 28	0.036	0	/ 20	0.000	0	/ 46	0.000
21. FSpOp	4	/ 27	0.148	4	/ 20	0.200	4	/ 46	0.087
22. FLPalAc	16	/ 28	0.571	12	/ 17	0.706	28	/ 41	0.683
23. TorPal *	0	/ 25	0.000	0	/ 19	0.000	0	/ 46	0.000
24. TorMax *	0	/ 29	0.000	0	/ 18	0.000	0	/ 46	0.000
25. FZyFAb	3	/ 28	0.107	1	/ 16	0.063	6	/ 45	0.133
26. FSupOrb	6	/ 28	0.214	2	/ 20	0.100	4	/ 47	0.085
27. FNotFr	5	/ 29	0.172	2	/ 22	0.091	8	/ 47	0.170
28. FAEthEx	10	/ 25	0.400	7	/ 19	0.368	21	/ 44	0.477
29. FPEthAb	1	/ 23	0.043	0	/ 18	0.000	2	/ 44	0.045
30. FIOrbAc	3	/ 27	0.111	0	/ 17	0.000	0	/ 45	0.000

* - Midline trait

TABLE A2.2.2 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - females.

LEFT SIDE ONLY.

	SEDMENT		BADARI		TEITA	
	trait present no.	freq.	trait present no.	freq.	trait present no.	freq.
31. OsInca *	0 / 29	0.000	0 / 21	0.000	1 / 47	0.021
32. SuIOrb	8 / 27	0.296	3 / 17	0.176	17 / 43	0.395
33. NasSill	29 / 29	1.000	16 / 19	0.842	17 / 47	0.362
34. FNasal	22 / 24	0.917	14 / 15	0.933	30 / 44	0.682
35. CribOrb	0 / 29	0.000	1 / 21	0.048	2 / 47	0.043
36. SpurTro	0 / 26	0.000	2 / 20	0.100	3 / 47	0.064
37. FosTro	3 / 26	0.115	6 / 20	0.300	20 / 47	0.426
38. GrFront	11 / 29	0.379	6 / 21	0.286	13 / 47	0.277
39. OsSqPar	0 / 29	0.000	0 / 19	0.000	1 / 47	0.021
40. SuJapTr	2 / 27	0.074	1 / 15	0.067	2 / 36	0.056
41. ProcMar	1 / 28	0.036	0 / 16	0.000	2 / 43	0.047
42. FZyTem	17 / 28	0.607	10 / 15	0.667	31 / 45	0.689
43. FZyOrb	25 / 28	0.893	12 / 15	0.800	43 / 46	0.935
44. OsOcMas	1 / 28	0.036	0 / 22	0.000	3 / 46	0.065
45. CanConI	7 / 27	0.259	7 / 20	0.350	12 / 44	0.273
46. TubConP	0 / 24	0.000	1 / 17	0.059	0 / 41	0.000
47. BrJugF	3 / 29	0.103	7 / 22	0.318	2 / 46	0.043
48. TubPhar *	7 / 29	0.241	3 / 19	0.158	2 / 47	0.043
49. FosPhar *	5 / 29	0.172	5 / 20	0.250	2 / 47	0.043
50. FOvOp	1 / 28	0.036	1 / 18	0.056	0 / 46	0.000
51. FVesal	6 / 29	0.207	2 / 17	0.118	3 / 43	0.070
52. BrPtBas	1 / 26	0.038	0 / 17	0.000	0 / 43	0.000
53. BrPtSp	1 / 26	0.038	1 / 15	0.067	0 / 40	0.000
54. BrSpBas	1 / 27	0.037	0 / 20	0.000	2 / 45	0.044
55. SpinFOv	3 / 29	0.103	0 / 18	0.000	2 / 46	0.043
56. FSpAc	1 / 27	0.037	1 / 20	0.050	1 / 45	0.022
57. PerfPt	0 / 25	0.000	0 / 13	0.000	1 / 36	0.028
58. SpurPt	8 / 15	0.533	2 / 7	0.286	13 / 26	0.500
59. BrPal	3 / 28	0.107	5 / 19	0.263	6 / 46	0.130
60. FZyFMu	9 / 25	0.360	6 / 15	0.400	12 / 39	0.308

* - Midline trait

APPENDIX 2

TABLE A2.3.1 .

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - males.

RIGHT SIDE ONLY.

	GIZA			KERMA			NAQADA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	25	/ 55	0.455	20	/ 43	0.465	30	/ 50	0.600
2. OsAtLam *	12	/ 55	0.218	2	/ 43	0.047	4	/ 50	0.080
3. OsLambd	25	/ 55	0.455	6	/ 43	0.140	16	/ 50	0.320
4. FPariet	32	/ 55	0.582	24	/ 43	0.558	22	/ 49	0.449
5. OsBreg *	0	/ 55	0.000	0	/ 43	0.000	1	/ 49	0.020
6. SuMetop *	0	/ 55	0.000	0	/ 43	0.000	1	/ 50	0.020
7. OsCoron	1	/ 55	0.018	0	/ 43	0.000	2	/ 49	0.041
8. OsPter	5	/ 55	0.091	3	/ 41	0.073	6	/ 50	0.120
9. FrTemAr	0	/ 55	0.000	3	/ 41	0.073	0	/ 50	0.000
10. OsPaNot	5	/ 55	0.091	3	/ 43	0.070	4	/ 50	0.080
11. OsAster	1	/ 55	0.018	0	/ 43	0.000	4	/ 50	0.080
12. TorAud	1	/ 55	0.018	0	/ 43	0.000	2	/ 50	0.040
13. FHusch	6	/ 55	0.109	4	/ 43	0.093	6	/ 50	0.120
14. FMasEx	17	/ 35	0.486	15	/ 25	0.600	12	/ 39	0.308
15. FMasAb	20	/ 55	0.364	18	/ 43	0.419	11	/ 50	0.220
16. CanConP	33	/ 55	0.600	23	/ 42	0.548	36	/ 50	0.720
17. BifaCon	0	/ 55	0.000	0	/ 41	0.000	0	/ 49	0.000
18. TubConA	7	/ 55	0.127	2	/ 43	0.047	7	/ 50	0.140
19. BrCanHy	13	/ 55	0.236	6	/ 43	0.140	11	/ 50	0.220
20. FOvSpOp	0	/ 55	0.000	0	/ 42	0.000	1	/ 50	0.020
21. FSpOp	6	/ 55	0.109	5	/ 42	0.119	8	/ 49	0.163
22. FLPalAc	50	/ 55	0.909	37	/ 43	0.860	43	/ 48	0.896
23. TorPal *	0	/ 55	0.000	0	/ 43	0.000	0	/ 50	0.000
24. TorMax	0	/ 55	0.000	0	/ 42	0.000	0	/ 49	0.000
25. FZyFAb	9	/ 55	0.164	8	/ 42	0.190	7	/ 50	0.140
26. FSupOrb	11	/ 55	0.200	4	/ 43	0.093	7	/ 50	0.140
27. FNotFr	6	/ 55	0.109	8	/ 43	0.186	6	/ 50	0.120
28. FAEthEx	14	/ 52	0.269	16	/ 39	0.410	16	/ 42	0.381
29. FPEthAb	0	/ 52	0.000	1	/ 38	0.026	5	/ 45	0.111
30. FlOrbAc	2	/ 55	0.036	2	/ 42	0.048	2	/ 49	0.041

* - Midline trait

APPENDIX 2

TABLE A2.3.1 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - males.

RIGHT SIDE ONLY.

	GIZA			KERMA			NAQADA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
31. OsInca *	2	/ 55	0.036	3	/ 43	0.070	2	/ 50	0.040
32. SuIOrb	14	/ 55	0.255	5	/ 42	0.119	17	/ 48	0.354
33. NasSill	41	/ 55	0.745	31	/ 42	0.738	44	/ 49	0.898
34. FNasal	44	/ 52	0.846	32	/ 34	0.941	37	/ 41	0.902
35. CribOrb	11	/ 55	0.200	2	/ 43	0.047	2	/ 50	0.040
36. SpurTro	4	/ 55	0.073	6	/ 42	0.143	6	/ 46	0.130
37. FosTro	12	/ 55	0.218	11	/ 42	0.262	14	/ 46	0.304
38. GrFront	11	/ 55	0.200	8	/ 43	0.186	20	/ 50	0.400
39. OsSqPar	1	/ 55	0.018	1	/ 42	0.024	3	/ 50	0.060
40. SuJapTr	5	/ 55	0.091	1	/ 42	0.024	5	/ 45	0.111
41. ProcMar	0	/ 55	0.000	6	/ 42	0.143	2	/ 49	0.041
42. FZyTem	38	/ 55	0.691	29	/ 42	0.690	38	/ 50	0.760
43. FZyOrb	51	/ 55	0.927	34	/ 42	0.810	47	/ 50	0.940
44. OsOcMas	1	/ 55	0.018	4	/ 42	0.095	1	/ 50	0.020
45. CanConI	35	/ 55	0.636	16	/ 43	0.372	30	/ 50	0.600
46. TubConP	0	/ 55	0.000	0	/ 40	0.000	0	/ 48	0.000
47. BrJugF	10	/ 55	0.182	9	/ 43	0.209	13	/ 50	0.260
48. TubPhar *	21	/ 55	0.382	18	/ 43	0.419	19	/ 49	0.388
49. FosPhar *	9	/ 55	0.164	9	/ 43	0.209	6	/ 49	0.122
50. FOvOp	1	/ 55	0.018	0	/ 43	0.000	2	/ 49	0.041
51. FVesal	8	/ 55	0.145	6	/ 43	0.140	8	/ 49	0.163
52. BrPtBas	4	/ 55	0.073	1	/ 43	0.023	3	/ 49	0.061
53. BrPtSp	2	/ 54	0.037	2	/ 43	0.047	1	/ 46	0.022
54. BrSpBas	8	/ 55	0.145	3	/ 41	0.073	1	/ 50	0.020
55. SpinFOv	5	/ 55	0.091	6	/ 42	0.143	0	/ 50	0.000
56. FSpAc	1	/ 55	0.018	0	/ 42	0.000	3	/ 50	0.060
57. PerfPt	4	/ 53	0.075	1	/ 38	0.026	1	/ 35	0.029
58. SpurPt	26	/ 51	0.510	15	/ 32	0.469	17	/ 24	0.708
59. BrPal	8	/ 55	0.145	8	/ 42	0.190	9	/ 50	0.180
60. FZyFMu	18	/ 46	0.391	16	/ 34	0.471	17	/ 43	0.395

* - Midline trait

APPENDIX 2

TABLE A2.3.2.

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - males.

RIGHT SIDE ONLY.

	SEDMENT			BADARI			TEITA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	23	/ 38	0.605	21	/ 36	0.583	15	/ 34	0.441
2. OsAtLam *	4	/ 39	0.103	3	/ 36	0.083	4	/ 34	0.118
3. OsLambd	14	/ 39	0.359	12	/ 36	0.333	10	/ 34	0.294
4. FPariet	13	/ 39	0.333	19	/ 36	0.528	13	/ 34	0.382
5. OsBreg *	0	/ 39	0.000	0	/ 36	0.000	0	/ 34	0.000
6. SuMetop *	2	/ 39	0.051	4	/ 35	0.114	1	/ 33	0.030
7. OsCoron	1	/ 38	0.026	1	/ 34	0.029	0	/ 34	0.000
8. OsPter	2	/ 38	0.053	5	/ 32	0.156	0	/ 33	0.000
9. FrTemAr	0	/ 38	0.000	0	/ 32	0.000	3	/ 34	0.088
10. OsPaNot	3	/ 39	0.077	7	/ 36	0.194	6	/ 34	0.176
11. OsAster	3	/ 39	0.077	2	/ 34	0.059	4	/ 34	0.118
12. TorAud	4	/ 38	0.105	1	/ 34	0.029	0	/ 34	0.000
13. FHusch	3	/ 37	0.081	5	/ 33	0.152	7	/ 33	0.212
14. FMasEx	9	/ 24	0.375	15	/ 24	0.625	9	/ 24	0.375
15. FMasAb	13	/ 37	0.351	10	/ 34	0.294	10	/ 34	0.294
16. CanConP	14	/ 36	0.389	18	/ 33	0.545	16	/ 32	0.500
17. BifaCon	0	/ 33	0.000	0	/ 31	0.000	0	/ 27	0.000
18. TubConA	9	/ 37	0.243	5	/ 32	0.156	1	/ 30	0.033
19. BrCanHy	7	/ 37	0.189	4	/ 33	0.121	3	/ 34	0.088
20. FOvSpOp	0	/ 38	0.000	0	/ 34	0.000	2	/ 34	0.059
21. FSpOp	6	/ 38	0.158	3	/ 32	0.094	5	/ 34	0.147
22. FLPalAc	31	/ 34	0.912	28	/ 31	0.903	29	/ 29	1.000
23. TorPal *	0	/ 36	0.000	0	/ 34	0.000	0	/ 33	0.000
24. TorMax	0	/ 38	0.000	0	/ 33	0.000	0	/ 34	0.000
25. FZyFAb	5	/ 38	0.132	6	/ 34	0.176	8	/ 31	0.258
26. FSupOrb	8	/ 39	0.205	7	/ 32	0.219	4	/ 34	0.118
27. FNotFr	6	/ 39	0.154	3	/ 34	0.088	4	/ 34	0.118
28. FAEthEx	8	/ 29	0.276	10	/ 25	0.400	14	/ 33	0.424
29. FPEthAb	0	/ 33	0.000	0	/ 25	0.000	0	/ 33	0.000
30. FIOrbAc	4	/ 33	0.121	2	/ 30	0.067	3	/ 32	0.094

* - Midline trait

APPENDIX 2

TABLE A2.3.2 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - males.

RIGHT SIDE ONLY.

	SEDMENT		BADARI		TEITA	
	trait present / no.	freq.	trait present / no.	freq.	trait present / no.	freq.
31. OsInca *	0 / 39	0.000	0 / 36	0.000	1 / 34	0.029
32. SuIOrb	5 / 33	0.152	10 / 30	0.333	6 / 31	0.194
33. NasSill	33 / 38	0.868	26 / 32	0.813	14 / 34	0.412
34. FNasal	22 / 31	0.710	21 / 28	0.750	28 / 30	0.933
35. CribOrb	2 / 39	0.051	1 / 35	0.029	2 / 34	0.059
36. SpurTro	3 / 33	0.091	2 / 30	0.067	2 / 34	0.059
37. FosTro	7 / 33	0.212	5 / 30	0.167	5 / 34	0.147
38. GrFront	6 / 39	0.154	9 / 35	0.257	13 / 34	0.382
39. OsSqPar	1 / 37	0.027	1 / 33	0.030	2 / 34	0.059
40. SuJapTr	2 / 32	0.063	4 / 30	0.133	3 / 30	0.100
41. ProcMar	3 / 38	0.079	0 / 34	0.000	2 / 31	0.065
42. FZyTem	28 / 38	0.737	23 / 33	0.697	28 / 33	0.848
43. FZyOrb	34 / 38	0.895	31 / 33	0.939	27 / 33	0.818
44. OsOcMas	1 / 37	0.027	3 / 34	0.088	2 / 34	0.059
45. CanConI	13 / 34	0.382	17 / 32	0.531	16 / 33	0.485
46. TubConP	1 / 35	0.029	1 / 29	0.034	0 / 34	0.000
47. BrJugF	7 / 36	0.194	9 / 31	0.290	3 / 34	0.088
48. TubPhar *	13 / 36	0.361	11 / 33	0.333	8 / 33	0.242
49. FosPhar *	6 / 36	0.167	5 / 33	0.152	3 / 33	0.091
50. FOvOp	1 / 38	0.026	0 / 31	0.000	1 / 34	0.029
51. FVesal	6 / 38	0.158	5 / 28	0.179	5 / 31	0.161
52. BrPtBas	3 / 38	0.079	2 / 31	0.065	1 / 31	0.032
53. BrPtSp	0 / 36	0.000	1 / 28	0.036	0 / 31	0.000
54. BrSpBas	3 / 38	0.079	3 / 31	0.097	1 / 34	0.029
55. SpinFOv	1 / 37	0.027	1 / 31	0.032	0 / 34	0.000
56. FSpAc	2 / 38	0.053	4 / 31	0.129	2 / 34	0.059
57. PerfPt	0 / 28	0.000	2 / 30	0.067	2 / 25	0.080
58. SpurPt	12 / 23	0.522	12 / 16	0.750	7 / 16	0.438
59. BrPal	5 / 37	0.135	6 / 31	0.194	6 / 31	0.194
60. FZyFMu	14 / 33	0.424	11 / 28	0.393	4 / 23	0.174

* - Midline trait

APPENDIX 2

TABLE A2.4.1.

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - females.

RIGHT SIDE ONLY.

	GIZA			KERMA			NAQADA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	18	/ 52	0.346	22	/ 41	0.537	31	/ 51	0.608
2. OsAtLam *	7	/ 51	0.137	3	/ 41	0.073	6	/ 51	0.118
3. OsLambd	20	/ 52	0.385	9	/ 41	0.220	17	/ 51	0.333
4. FPariet	23	/ 52	0.442	25	/ 41	0.610	26	/ 51	0.510
5. OsBreg *	1	/ 52	0.019	1	/ 41	0.024	1	/ 51	0.020
6. SuMetop *	1	/ 52	0.019	2	/ 41	0.049	1	/ 50	0.020
7. OsCoron	2	/ 52	0.038	0	/ 41	0.000	2	/ 51	0.039
8. OsPter	6	/ 52	0.115	7	/ 40	0.175	9	/ 51	0.176
9. FrTemAr	0	/ 52	0.000	3	/ 40	0.075	1	/ 51	0.020
10. OsPaNot	3	/ 52	0.058	4	/ 41	0.098	5	/ 51	0.098
11. OsAster	3	/ 52	0.058	5	/ 41	0.122	2	/ 51	0.039
12. TorAud	0	/ 52	0.000	1	/ 41	0.024	0	/ 51	0.000
13. FHusch	14	/ 51	0.275	13	/ 40	0.325	7	/ 50	0.140
14. FMasEx	18	/ 26	0.692	11	/ 17	0.647	14	/ 27	0.519
15. FMasAb	26	/ 52	0.500	24	/ 41	0.585	24	/ 51	0.471
16. CanConP	33	/ 52	0.635	25	/ 34	0.735	33	/ 51	0.647
17. BifaCon	0	/ 52	0.000	0	/ 37	0.000	0	/ 50	0.000
18. TubConA	6	/ 52	0.115	5	/ 40	0.125	7	/ 51	0.137
19. BrCanHy	11	/ 52	0.212	1	/ 39	0.026	6	/ 51	0.118
20. FOvSpOp	1	/ 52	0.019	0	/ 41	0.000	2	/ 51	0.039
21. FSpOp	10	/ 52	0.192	5	/ 41	0.122	4	/ 51	0.078
22. FLPalAc	48	/ 52	0.923	30	/ 39	0.769	41	/ 51	0.804
23. TorPal *	0	/ 52	0.000	0	/ 39	0.000	0	/ 50	0.000
24. TorMax	0	/ 52	0.000	0	/ 40	0.000	0	/ 50	0.000
25. FZyFAb	12	/ 52	0.231	9	/ 41	0.220	9	/ 51	0.176
26. FSupOrb	7	/ 52	0.135	7	/ 41	0.171	10	/ 50	0.200
27. FNotFr	3	/ 52	0.058	6	/ 41	0.146	2	/ 51	0.039
28. FAEthEx	20	/ 51	0.392	12	/ 39	0.308	19	/ 48	0.396
29. FPEthAb	2	/ 51	0.039	1	/ 38	0.026	0	/ 48	0.000
30. FlOrbAc	7	/ 52	0.135	0	/ 40	0.000	3	/ 51	0.059

* - Midline trait

APPENDIX 2

TABLE A2.4.1 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - females.

RIGHT SIDE ONLY.

	GIZA		KERMA		NAQADA	
	trait present no.	freq.	trait present no.	freq.	trait present no.	freq.
31. OsInca *	1 / 52	0.019	0 / 41	0.000	0 / 51	0.000
32. SulOrb	23 / 52	0.442	8 / 40	0.200	21 / 51	0.412
33. NasSill	46 / 52	0.885	19 / 41	0.463	41 / 50	0.820
34. FNasal	43 / 50	0.860	24 / 30	0.800	36 / 40	0.900
35. CribOrb	4 / 52	0.077	4 / 41	0.098	2 / 51	0.039
36. SpurTro	10 / 52	0.192	6 / 41	0.146	7 / 50	0.140
37. FosTro	11 / 52	0.212	8 / 41	0.195	18 / 50	0.360
38. GrFront	12 / 52	0.231	13 / 41	0.317	13 / 51	0.255
39. OsSqPar	2 / 52	0.038	1 / 40	0.025	3 / 51	0.059
40. SuJapTr	6 / 52	0.115	0 / 41	0.000	0 / 48	0.000
41. ProcMar	3 / 52	0.058	3 / 41	0.073	2 / 51	0.039
42. FZyTem	35 / 52	0.673	32 / 41	0.780	35 / 51	0.686
43. FZyOrb	43 / 52	0.827	33 / 41	0.805	49 / 51	0.961
44. OsOcMas	0 / 51	0.000	1 / 40	0.025	2 / 51	0.039
45. CanConI	31 / 52	0.596	13 / 37	0.351	26 / 51	0.510
46. TubConP	1 / 52	0.019	0 / 38	0.000	0 / 49	0.000
47. BrJugF	9 / 52	0.173	10 / 39	0.256	8 / 51	0.157
48. TubPhar *	12 / 52	0.231	12 / 41	0.293	11 / 51	0.216
49. FosPhar *	10 / 52	0.192	11 / 41	0.268	13 / 51	0.255
50. FOvOp	2 / 52	0.038	0 / 41	0.000	0 / 50	0.000
51. FVesal	12 / 52	0.231	11 / 41	0.268	8 / 50	0.160
52. BrPtBas	2 / 52	0.038	4 / 41	0.098	1 / 51	0.020
53. BrPtSp	0 / 51	0.000	1 / 41	0.024	0 / 50	0.000
54. BrSpBas	3 / 52	0.058	4 / 41	0.098	2 / 51	0.039
55. SpinFOv	3 / 52	0.058	5 / 41	0.122	1 / 51	0.020
56. FSpAc	2 / 52	0.038	0 / 41	0.000	1 / 51	0.020
57. PerfPt	2 / 50	0.040	2 / 32	0.063	3 / 44	0.068
58. SpurPt	30 / 49	0.612	15 / 31	0.484	17 / 37	0.459
59. BrPal	9 / 52	0.173	10 / 40	0.250	11 / 50	0.220
60. FZyFMu	16 / 40	0.400	20 / 32	0.625	16 / 42	0.381

* - Midline trait

APPENDIX 2

TABLE A2.4.2 .

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - females.

RIGHT SIDE ONLY.

	SEDMENT			BADARI			TEITA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	18	/ 29	0.621	9	/ 20	0.450	19	/ 47	0.404
2. OsAtLam *	6	/ 29	0.207	3	/ 21	0.143	8	/ 47	0.170
3. OsLambd	10	/ 29	0.345	7	/ 20	0.350	24	/ 47	0.511
4. FPariet	11	/ 29	0.379	6	/ 21	0.286	27	/ 47	0.574
5. OsBreg *	0	/ 29	0.000	0	/ 21	0.000	0	/ 47	0.000
6. SuMetop *	1	/ 28	0.036	0	/ 21	0.000	0	/ 47	0.000
7. OsCoron	2	/ 29	0.069	0	/ 19	0.000	0	/ 47	0.000
8. OsPter	8	/ 29	0.276	2	/ 18	0.111	6	/ 45	0.133
9. FrTemAr	1	/ 29	0.034	3	/ 18	0.167	2	/ 46	0.043
10. OsPaNot	7	/ 29	0.241	1	/ 20	0.050	10	/ 47	0.213
11. OsAster	3	/ 29	0.103	2	/ 20	0.100	1	/ 47	0.021
12. TorAud	2	/ 29	0.069	1	/ 21	0.048	0	/ 47	0.000
13. FHusch	6	/ 28	0.214	5	/ 22	0.227	16	/ 47	0.340
14. FMasEx	7	/ 15	0.467	8	/ 12	0.667	7	/ 23	0.304
15. FMasAb	14	/ 29	0.483	8	/ 20	0.400	23	/ 46	0.500
16. CanConP	15	/ 28	0.536	12	/ 19	0.632	24	/ 46	0.522
17. BifaCon	0	/ 27	0.000	1	/ 17	0.059	0	/ 36	0.000
18. TubConA	1	/ 29	0.034	1	/ 17	0.059	1	/ 47	0.021
19. BrCanHy	3	/ 29	0.103	3	/ 21	0.143	2	/ 47	0.043
20. FOvSpOp	1	/ 29	0.034	0	/ 20	0.000	2	/ 46	0.043
21. FSpOp	11	/ 29	0.379	4	/ 20	0.200	8	/ 46	0.174
22. FLPalAc	20	/ 27	0.741	14	/ 17	0.824	31	/ 42	0.738
23. TorPal *	0	/ 25	0.000	0	/ 19	0.000	0	/ 46	0.000
24. TorMax	0	/ 28	0.000	0	/ 19	0.000	0	/ 47	0.000
25. FZyFAb	3	/ 28	0.107	1	/ 17	0.059	10	/ 45	0.222
26. FSupOrb	4	/ 29	0.138	7	/ 20	0.350	4	/ 47	0.085
27. FNotFr	6	/ 29	0.207	1	/ 21	0.048	6	/ 46	0.130
28. FAEthEx	10	/ 25	0.400	4	/ 13	0.308	21	/ 43	0.488
29. FPEthAb	0	/ 24	0.000	0	/ 16	0.000	1	/ 45	0.022
30. FIOrbAc	3	/ 27	0.111	0	/ 16	0.000	3	/ 44	0.068

* - Midline trait

APPENDIX 2

TABLE A2.4.2 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

6 African groups - females.

RIGHT SIDE ONLY.

	SEDMENT			BADARI			TEITA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
31. OsInca *	0	/ 29	0.000	0	/ 21	0.000	1	/ 47	0.021
32. SuIOrb	9	/ 28	0.321	3	/ 16	0.188	17	/ 44	0.386
33. NasSill	27	/ 28	0.964	17	/ 21	0.810	14	/ 46	0.304
34. FNasal	20	/ 21	0.952	12	/ 13	0.923	36	/ 44	0.818
35. CribOrb	0	/ 29	0.000	2	/ 20	0.100	2	/ 47	0.043
36. SpurTro	1	/ 28	0.036	1	/ 20	0.050	8	/ 45	0.178
37. FosTro	1	/ 28	0.036	6	/ 20	0.300	21	/ 46	0.457
38. GrFront	14	/ 29	0.483	6	/ 19	0.316	13	/ 47	0.277
39. OsSqPar	3	/ 29	0.103	0	/ 17	0.000	2	/ 47	0.043
40. SuJapTr	3	/ 26	0.115	2	/ 14	0.143	3	/ 39	0.077
41. ProcMar	1	/ 28	0.036	0	/ 17	0.000	3	/ 43	0.070
42. FZyTem	20	/ 28	0.714	12	/ 17	0.706	34	/ 46	0.739
43. FZyOrb	27	/ 28	0.964	16	/ 17	0.941	37	/ 47	0.787
44. OsOcMas	2	/ 29	0.069	1	/ 19	0.053	8	/ 47	0.170
45. CanConI	11	/ 27	0.407	7	/ 17	0.412	12	/ 46	0.261
46. TubConP	0	/ 24	0.000	1	/ 16	0.063	0	/ 42	0.000
47. BrJugF	4	/ 29	0.138	5	/ 18	0.278	4	/ 47	0.085
48. TubPhar *	7	/ 29	0.241	3	/ 19	0.158	2	/ 47	0.043
49. FosPhar *	5	/ 29	0.172	5	/ 20	0.250	2	/ 47	0.043
50. FOvOp	2	/ 28	0.071	0	/ 18	0.000	0	/ 47	0.000
51. FVesal	5	/ 28	0.179	4	/ 18	0.222	6	/ 46	0.130
52. BrPtBas	0	/ 28	0.000	1	/ 19	0.053	1	/ 46	0.022
53. BrPtSp	1	/ 27	0.037	0	/ 14	0.000	0	/ 43	0.000
54. BrSpBas	0	/ 29	0.000	1	/ 21	0.048	1	/ 46	0.022
55. SpinFOv	0	/ 29	0.000	0	/ 17	0.000	1	/ 47	0.021
56. FSpAc	1	/ 29	0.034	0	/ 19	0.000	2	/ 46	0.043
57. PerfPt	2	/ 23	0.087	0	/ 11	0.000	1	/ 39	0.026
58. SpurPt	4	/ 17	0.235	5	/ 6	0.833	16	/ 30	0.533
59. BrPal	2	/ 27	0.074	5	/ 20	0.250	12	/ 47	0.255
60. FZyFMu	12	/ 25	0.480	4	/ 16	0.250	11	/ 35	0.314

* - Midline trait

APPENDIX 2

TABLE A2.5.1.

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

LEFT SIDE ONLY.

	SINDOS			PIERIA			LERNA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	10	/ 29	0.345	4	/ 26	0.154	6	/ 31	0.194
2. OsAtLam *	1	/ 27	0.037	6	/ 25	0.240	1	/ 26	0.038
3. OsLambd	9	/ 30	0.300	12	/ 26	0.462	9	/ 25	0.360
4. FPariet	1	/ 25	0.040	2	/ 25	0.080	5	/ 29	0.172
5. OsBreg *	0	/ 27	0.000	0	/ 25	0.000	0	/ 33	0.000
6. SuMetop *	1	/ 33	0.030	1	/ 26	0.038	3	/ 36	0.083
7. OsCoron	0	/ 29	0.000	1	/ 25	0.040	1	/ 31	0.032
8. OsPter	2	/ 19	0.105	3	/ 22	0.136	0	/ 24	0.000
9. FrTemAr	0	/ 20	0.000	1	/ 22	0.045	0	/ 28	0.000
10. OsPaNot	4	/ 27	0.148	4	/ 26	0.154	2	/ 26	0.077
11. OsAster	3	/ 26	0.115	4	/ 26	0.154	3	/ 26	0.115
12. TorAud	0	/ 29	0.000	1	/ 26	0.038	0	/ 31	0.000
13. FHusch	8	/ 28	0.286	4	/ 26	0.154	7	/ 31	0.226
14. FMasEx	12	/ 22	0.545	11	/ 16	0.688	12	/ 16	0.750
15. FMasAb	8	/ 29	0.276	10	/ 26	0.385	8	/ 24	0.333
16. CanConP	13	/ 23	0.565	10	/ 18	0.556	13	/ 16	0.813
17. BifaCon	2	/ 20	0.100	0	/ 18	0.000	0	/ 17	0.000
18. TubConA	5	/ 23	0.217	5	/ 23	0.217	1	/ 14	0.071
19. BrCanHy	3	/ 25	0.120	4	/ 22	0.182	5	/ 16	0.313
20. FOvSpOp	0	/ 24	0.000	1	/ 22	0.045	0	/ 22	0.000
21. FSpOp	7	/ 24	0.292	8	/ 22	0.364	4	/ 17	0.235
22. FLPalAc	12	/ 15	0.800	14	/ 16	0.875	16	/ 18	0.889
23. TorPal *	2	/ 20	0.100	1	/ 20	0.050	0	/ 19	0.000
24. TorMax	0	/ 22	0.000	0	/ 17	0.000	0	/ 35	0.000
25. FZyFAb	9	/ 23	0.391	4	/ 19	0.211	10	/ 33	0.303
26. FSupOrb	4	/ 25	0.160	7	/ 24	0.292	5	/ 26	0.192
27. FNotFr	1	/ 26	0.038	4	/ 26	0.154	5	/ 31	0.161
28. FAEthEx	5	/ 13	0.385	5	/ 14	0.357	4	/ 8	0.500
29. FPEthAb	0	/ 13	0.000	0	/ 16	0.000	1	/ 9	0.111
30. FIOrbAc	2	/ 17	0.118	4	/ 19	0.211	6	/ 21	0.286

* - Midline trait

TABLE A2.5.1 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

LEFT SIDE ONLY.

	SINDOS			PIERIA			LERNA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
31. OsInca *	1	/ 29	0.034	1	/ 26	0.038	0	/ 26	0.000
32. SulOrb	7	/ 16	0.438	10	/ 20	0.500	5	/ 19	0.263
33. NasSill	14	/ 21	0.667	15	/ 20	0.750	25	/ 33	0.758
34. FNasal	9	/ 12	0.750	15	/ 17	0.882	13	/ 18	0.722
35. CribOrb	2	/ 27	0.074	3	/ 23	0.130	1	/ 30	0.033
36. SpurTro	2	/ 21	0.095	5	/ 22	0.227	2	/ 21	0.095
37. FosTro	5	/ 21	0.238	2	/ 22	0.091	2	/ 22	0.091
38. GrFront	7	/ 29	0.241	5	/ 26	0.192	8	/ 34	0.235
39. OsSqPar	0	/ 23	0.000	1	/ 23	0.043	0	/ 28	0.000
40. SuJapTr	0	/ 21	0.000	1	/ 16	0.063	0	/ 27	0.000
41. ProcMar	9	/ 21	0.429	8	/ 20	0.400	7	/ 34	0.206
42. FZyTem	17	/ 22	0.773	17	/ 19	0.895	23	/ 33	0.697
43. FZyOrb	13	/ 22	0.591	13	/ 20	0.650	23	/ 34	0.676
44. OsOcMas	0	/ 27	0.000	1	/ 25	0.040	0	/ 21	0.000
45. CanConI	0	/ 24	0.000	0	/ 20	0.000	1	/ 12	0.083
46. TubConP	3	/ 25	0.120	0	/ 20	0.000	2	/ 20	0.100
47. BrJugF	0	/ 19	0.000	0	/ 21	0.000	0	/ 16	0.000
48. TubPhar *	10	/ 27	0.370	9	/ 21	0.429	4	/ 15	0.267
49. FosPhar *	3	/ 27	0.111	4	/ 21	0.190	1	/ 16	0.063
50. FOvOp	0	/ 22	0.000	0	/ 19	0.000	0	/ 16	0.000
51. FVesal	9	/ 24	0.375	12	/ 22	0.545	10	/ 20	0.500
52. BrPtBas	1	/ 22	0.045	1	/ 21	0.048	0	/ 18	0.000
53. BrPtSp	0	/ 21	0.000	2	/ 20	0.100	3	/ 15	0.200
54. BrSpBas	1	/ 25	0.040	1	/ 22	0.045	1	/ 18	0.056
55. SpinFOv	1	/ 21	0.048	0	/ 21	0.000	0	/ 19	0.000
56. FSpAc	0	/ 22	0.000	0	/ 21	0.000	2	/ 20	0.100
57. PerfPt	1	/ 12	0.083	1	/ 14	0.071	0	/ 5	0.000
58. SpurPt	8	/ 12	0.667	5	/ 14	0.357	5	/ 8	0.625
59. BrPal	0	/ 23	0.000	0	/ 19	0.000	1	/ 23	0.043
60. FZyFMu	5	/ 14	0.357	7	/ 15	0.467	12	/ 23	0.522

* - Midline trait

APPENDIX 2

TABLE A2.5.2.

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooledsexes.

LEFT SIDE ONLY.

	ATHENS-M			ATHENS-G		
	trait present	no.	freq.	trait present	no.	freq.
..1. HiNuLin	13	/ 26	0.500	8	/ 18	0.444
..2. OsAtLam *	3	/ 26	0.115	3	/ 19	0.158
..3. OsLambd	7	/ 27	0.259	5	/ 20	0.250
..4. FPariet	5	/ 28	0.179	1	/ 18	0.056
..5. OsBreg *	0	/ 28	0.000	0	/ 19	0.000
..6. SuMetop *	2	/ 28	0.071	1	/ 20	0.050
..7. OsCoron	0	/ 27	0.000	0	/ 17	0.000
..8. OsPter	0	/ 23	0.000	2	/ 13	0.154
..9. FrTemAr	1	/ 25	0.040	0	/ 16	0.000
10. OsPaNot	3	/ 22	0.136	2	/ 14	0.143
11. OsAster	3	/ 25	0.120	3	/ 19	0.158
12. TorAud	0	/ 28	0.000	0	/ 20	0.000
13. FHusch	7	/ 27	0.259	1	/ 18	0.056
14. FMasEx	9	/ 23	0.391	5	/ 12	0.417
15. FMasAb	5	/ 28	0.179	8	/ 20	0.400
16. CanConP	9	/ 17	0.529	7	/ 15	0.467
17. BifaCon	1	/ 21	0.048	0	/ 16	0.000
18. TubConA	7	/ 22	0.318	3	/ 16	0.188
19. BrCanHy	6	/ 24	0.250	0	/ 17	0.000
20. FOvSpOp	0	/ 18	0.000	0	/ 16	0.000
21. FSpOp	0	/ 15	0.000	1	/ 14	0.071
22. FLPalAc	9	/ 12	0.750	8	/ 13	0.615
23. TorPal *	0	/ 18	0.000	0	/ 16	0.000
24. TorMax	0	/ 21	0.000	0	/ 15	0.000
25. FZyFAb	5	/ 22	0.227	3	/ 14	0.214
26. FSupOrb	8	/ 27	0.296	5	/ 17	0.294
27. FNotFr	3	/ 24	0.125	0	/ 18	0.000
28. FAEthEx	4	/ 8	0.500	1	/ 3	0.333
29. FPEthAb	0	/ 11	0.000	0	/ 4	0.000
30. FIOrbAc	1	/ 11	0.091	1	/ 8	0.125

* - Midline trait

TABLE A2.5.2 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooledsexes.

LEFT SIDE ONLY.

	ATHENS-M		ATHENS-G	
	trait present no.	freq.	trait present no.	freq.
31. OsInca *	0 / 28	0.000	0 / 19	0.000
32. SuIOrb	6 / 16	0.375	6 / 10	0.600
33. NasSill	15 / 20	0.750	10 / 16	0.625
34. FNasal	9 / 13	0.692	5 / 10	0.500
35. CribOrb	2 / 24	0.083	0 / 17	0.000
36. SpurTro	2 / 19	0.105	1 / 9	0.111
37. FosTro	6 / 21	0.286	4 / 10	0.400
38. GrFront	3 / 28	0.107	1 / 20	0.050
39. OsSqPar	0 / 23	0.000	0 / 17	0.000
40. SuJapTr	0 / 18	0.000	0 / 12	0.000
41. ProcMar	5 / 22	0.227	3 / 13	0.231
42. FZyTem	15 / 23	0.652	10 / 14	0.714
43. FZyOrb	19 / 22	0.864	13 / 14	0.929
44. OsOcMas	0 / 22	0.000	2 / 19	0.105
45. CanConI	3 / 20	0.150	3 / 16	0.188
46. TubConP	0 / 16	0.000	0 / 17	0.000
47. BrJugF	1 / 20	0.050	0 / 16	0.000
48. TubPhar *	6 / 24	0.250	3 / 17	0.176
49. FosPhar *	6 / 24	0.250	2 / 17	0.118
50. FOvOp	0 / 18	0.000	0 / 12	0.000
51. FVesal	13 / 23	0.565	5 / 14	0.357
52. BrPtBas	1 / 21	0.048	0 / 12	0.000
53. BrPtSp	1 / 20	0.050	0 / 11	0.000
54. BrSpBas	1 / 17	0.059	1 / 14	0.071
55. SpinFOv	4 / 18	0.222	2 / 14	0.143
56. FSpAc	1 / 18	0.056	1 / 14	0.071
57. PerfPt	0 / 6	0.000	3 / 6	0.500
58. SpurPt	3 / 6	0.500	1 / 5	0.200
59. BrPal	2 / 19	0.105	1 / 15	0.067
60. FZyFMu	8 / 17	0.471	5 / 11	0.455

* - Midline trait

APPENDIX 2

TABLE A2.5.3.

NON-METRIC TRAITS : RAW FREQUENCIES.

13 Greek and African groups - pooledsexes.

LEFT SIDE ONLY.

	FORTETSA		PYRGOS	
	trait present no.	freq.	trait present no.	freq.
1. HiNuLin	4 / 10	0.400	12 / 19	0.632
2. OsAtLam *	2 / 11	0.182	0 / 21	0.000
3. OsLambd	1 / 11	0.091	7 / 23	0.304
4. FPariet	1 / 10	0.100	10 / 23	0.435
5. OsBreg *	0 / 11	0.000	0 / 25	0.000
6. SuMetop *	0 / 11	0.000	3 / 24	0.125
7. OsCoron	0 / 11	0.000	0 / 22	0.000
8. OsPter	3 / 8	0.375	0 / 12	0.000
9. FrTemAr	0 / 9	0.000	1 / 12	0.083
10. OsPaNot	2 / 10	0.200	1 / 17	0.059
11. OsAster	1 / 11	0.091	0 / 19	0.000
12. TorAud	0 / 10	0.000	1 / 19	0.053
13. FHusch	2 / 10	0.200	1 / 16	0.063
14. FMasEx	4 / 7	0.571	10 / 12	0.833
15. FMasAb	3 / 10	0.300	5 / 17	0.294
16. CanConP	5 / 9	0.556	5 / 7	0.714
17. BifaCon	0 / 9	0.000	0 / 9	0.000
18. TubConA	2 / 7	0.286	0 / 9	0.000
19. BrCanHy	0 / 10	0.000	3 / 10	0.300
20. FOvSpOp	0 / 9	0.000	0 / 13	0.000
21. FSpOp	3 / 9	0.333	3 / 11	0.273
22. FLPalAc	5 / 6	0.833	3 / 3	1.000
23. TorPal *	0 / 6	0.000	1 / 5	0.200
24. TorMax	0 / 6	0.000	0 / 5	0.000
25. FZyFAb	2 / 10	0.200	1 / 10	0.100
26. FSupOrb	2 / 9	0.222	2 / 21	0.095
27. FNotFr	1 / 10	0.100	4 / 21	0.190
28. FAEthEx	1 / 5	0.200	1 / 1	1.000
29. FPEthAb	0 / 6	0.000	0 / 0	9.999
30. FIOrbAc	0 / 7	0.000	0 / 4	0.000

* - Midline trait

TABLE A2.5.3 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooledsexes.

LEFT SIDE ONLY.

	FORTETSA		PYRGOS	
	trait present no.	freq.	trait present no.	freq.
31. OsInca *	0 / 11	0.000	2 / 21	0.095
32. SuIOrb	3 / 6	0.500	4 / 5	0.800
33. NasSill	5 / 7	0.714	5 / 6	0.833
34. FNasal	3 / 4	0.750	5 / 5	1.000
35. CribOrb	1 / 10	0.100	3 / 17	0.176
36. SpurTro	0 / 7	0.000	0 / 12	0.000
37. FosTro	4 / 7	0.571	3 / 13	0.231
38. GrFront	0 / 11	0.000	5 / 22	0.227
39. OsSqPar	0 / 10	0.000	0 / 12	0.000
40. SuJapTr	0 / 9	0.000	1 / 8	0.125
41. ProcMar	3 / 10	0.300	3 / 12	0.250
42. FZyTem	7 / 10	0.700	8 / 11	0.727
43. FZyOrb	9 / 10	0.900	9 / 10	0.900
44. OsOcMas	0 / 10	0.000	0 / 14	0.000
45. CanConI	2 / 9	0.222	0 / 9	0.000
46. TubConP	0 / 7	0.000	1 / 7	0.143
47. BrJugF	1 / 9	0.111	0 / 5	0.000
48. TubPhar *	1 / 8	0.125	3 / 9	0.333
49. FosPhar *	3 / 8	0.375	3 / 9	0.333
50. FOvOp	0 / 9	0.000	0 / 11	0.000
51. FVesal	3 / 9	0.333	5 / 8	0.625
52. BrPtBas	0 / 9	0.000	0 / 12	0.000
53. BrPtSp	1 / 9	0.111	0 / 11	0.000
54. BrSpBas	1 / 9	0.111	2 / 14	0.143
55. SpinFOv	0 / 8	0.000	1 / 12	0.083
56. FSpAc	0 / 9	0.000	1 / 12	0.083
57. PerfPt	1 / 1	1.000	0 / 3	0.000
58. SpurPt	1 / 1	1.000	4 / 4	1.000
59. BrPal	0 / 7	0.000	0 / 5	0.000
60. FZyFMu	3 / 7	0.429	1 / 9	0.111

* - Midline trait

APPENDIX 2

TABLE A2.5.4.

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

LEFT SIDE ONLY.

	GIZA		KERMA		NAQADA	
	trait present / no.	freq.	trait present / no.	freq.	trait present / no.	freq.
1. HiNuLin	45 / 107	0.421	43 / 84	0.512	60 / 100	0.600
2. OsAtLam *	19 / 106	0.179	5 / 84	0.060	10 / 101	0.099
3. OsLambd	36 / 106	0.340	28 / 84	0.333	36 / 101	0.356
4. FPariet	42 / 107	0.393	39 / 84	0.464	49 / 100	0.490
5. OsBreg *	1 / 107	0.009	1 / 84	0.012	2 / 100	0.020
6. SuMetop *	1 / 107	0.009	2 / 84	0.024	2 / 100	0.020
7. OsCoron	1 / 107	0.009	2 / 84	0.024	3 / 101	0.030
8. OsPter	9 / 107	0.084	9 / 82	0.110	16 / 99	0.162
9. FrTemAr	1 / 107	0.009	8 / 82	0.098	1 / 100	0.010
10. OsPaNot	7 / 107	0.065	9 / 82	0.110	8 / 101	0.079
11. OsAster	4 / 107	0.037	3 / 84	0.036	6 / 101	0.059
12. TorAud	1 / 107	0.009	0 / 84	0.000	2 / 100	0.020
13. FHusch	19 / 107	0.178	17 / 82	0.207	13 / 98	0.133
14. FMasEx	30 / 67	0.448	17 / 38	0.447	26 / 59	0.441
15. FMasAb	40 / 107	0.374	46 / 84	0.548	42 / 101	0.416
16. CanConP	63 / 107	0.589	48 / 79	0.608	64 / 100	0.640
17. BifaCon	1 / 106	0.009	0 / 82	0.000	0 / 96	0.000
18. TubConA	20 / 107	0.187	11 / 84	0.131	20 / 100	0.200
19. BrCanHy	25 / 107	0.234	16 / 83	0.193	18 / 100	0.180
20. FOvSpOp	0 / 107	0.000	2 / 84	0.024	1 / 100	0.010
21. FSpOp	10 / 107	0.093	10 / 83	0.120	13 / 99	0.131
22. FLPalAc	92 / 107	0.860	66 / 83	0.795	88 / 98	0.898
23. TorPal *	0 / 107	0.000	0 / 82	0.000	0 / 100	0.000
24. TorMax	0 / 107	0.000	0 / 84	0.000	0 / 101	0.000
25. FZyFAb	26 / 107	0.243	19 / 83	0.229	17 / 99	0.172
26. FSupOrb	20 / 107	0.187	16 / 83	0.193	18 / 101	0.178
27. FNotFr	9 / 107	0.084	9 / 83	0.108	7 / 100	0.070
28. FAEthEx	35 / 104	0.337	25 / 75	0.333	39 / 90	0.433
29. FPEthAb	3 / 104	0.029	1 / 75	0.013	2 / 89	0.022
30. FlOrbAc	14 / 107	0.131	3 / 83	0.036	9 / 100	0.090

* - Midline trait

TABLE A2.5.4 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

LEFT SIDE ONLY.

	GIZA		KERMA		NAQADA	
	trait present no.	freq.	trait present no.	freq.	trait present no.	freq.
31. OsInca *	3 / 107	0.028	3 / 84	0.036	2 / 101	0.020
32. SuIOrb	28 / 107	0.262	20 / 83	0.241	44 / 99	0.444
33. NasSill	90 / 107	0.841	54 / 84	0.643	85 / 98	0.867
34. FNasal	89 / 105	0.848	63 / 67	0.940	74 / 81	0.914
35. CribOrb	16 / 107	0.150	5 / 84	0.060	7 / 101	0.069
36. SpurTro	11 / 107	0.103	8 / 82	0.098	12 / 99	0.121
37. FosTro	29 / 107	0.271	18 / 82	0.220	45 / 99	0.455
38. GrFront	22 / 107	0.206	23 / 84	0.274	28 / 100	0.280
39. OsSqPar	3 / 107	0.028	3 / 82	0.037	5 / 99	0.051
40. SuJapTr	8 / 107	0.075	1 / 83	0.012	11 / 94	0.117
41. ProcMar	3 / 107	0.028	10 / 84	0.119	5 / 99	0.051
42. FZyTem	70 / 106	0.660	60 / 83	0.723	76 / 100	0.760
43. FZyOrb	99 / 107	0.925	71 / 82	0.866	90 / 100	0.900
44. OsOcMas	0 / 107	0.000	6 / 83	0.072	7 / 101	0.069
45. CanConI	49 / 107	0.458	30 / 83	0.361	53 / 100	0.530
46. TubConP	0 / 107	0.000	0 / 77	0.000	0 / 97	0.000
47. BrJugF	15 / 107	0.140	12 / 83	0.145	19 / 100	0.190
48. TubPhar *	33 / 107	0.308	30 / 84	0.357	30 / 100	0.300
49. FosPhar *	19 / 107	0.178	20 / 84	0.238	19 / 100	0.190
50. FOvOp	1 / 107	0.009	2 / 83	0.024	1 / 101	0.010
51. FVesal	15 / 107	0.140	17 / 82	0.207	17 / 101	0.168
52. BrPtBas	3 / 107	0.028	3 / 84	0.036	2 / 99	0.020
53. BrPtSp	2 / 107	0.019	0 / 83	0.000	3 / 93	0.032
54. BrSpBas	11 / 107	0.103	5 / 84	0.060	8 / 98	0.082
55. SpinFOv	2 / 107	0.019	8 / 84	0.095	5 / 101	0.050
56. FSpAc	5 / 107	0.047	4 / 84	0.048	3 / 99	0.030
57. PerfPt	12 / 105	0.114	0 / 68	0.000	9 / 84	0.107
58. SpurPt	74 / 104	0.712	28 / 61	0.459	43 / 67	0.642
59. BrPal	19 / 107	0.178	17 / 84	0.202	22 / 101	0.218
60. FZyFMu	29 / 81	0.358	28 / 64	0.438	26 / 82	0.317

* - Midline trait

APPENDIX 2

TABLE A2.5.5.

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

LEFT SIDE ONLY.

	SEDMENT			BADARI			TEITA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	39	/ 67	0.582	30	/ 56	0.536	36	/ 81	0.444
2. OsAtLam *	10	/ 68	0.147	6	/ 57	0.105	12	/ 81	0.148
3. OsLambd	26	/ 68	0.382	21	/ 57	0.368	32	/ 81	0.395
4. FPariet	23	/ 68	0.338	26	/ 57	0.456	31	/ 81	0.383
5. OsBreg *	0	/ 68	0.000	0	/ 57	0.000	0	/ 81	0.000
6. SuMetop *	3	/ 67	0.045	4	/ 56	0.071	1	/ 80	0.012
7. OsCoron	3	/ 67	0.045	1	/ 55	0.018	0	/ 81	0.000
8. OsPter	11	/ 67	0.164	11	/ 52	0.212	4	/ 79	0.051
9. FrTemAr	0	/ 67	0.000	2	/ 52	0.038	6	/ 81	0.074
10. OsPaNot	5	/ 67	0.075	8	/ 57	0.140	14	/ 81	0.173
11. OsAster	5	/ 68	0.074	5	/ 55	0.091	8	/ 80	0.100
12. TorAud	6	/ 67	0.090	2	/ 56	0.036	0	/ 81	0.000
13. FHusch	11	/ 64	0.172	10	/ 55	0.182	27	/ 80	0.337
14. FMasEx	18	/ 39	0.462	24	/ 38	0.632	16	/ 48	0.333
15. FMasAb	26	/ 65	0.400	18	/ 56	0.321	32	/ 80	0.400
16. CanConP	29	/ 65	0.446	28	/ 53	0.528	47	/ 78	0.603
17. BifaCon	0	/ 61	0.000	2	/ 46	0.043	0	/ 64	0.000
18. TubConA	10	/ 66	0.152	5	/ 47	0.106	3	/ 76	0.039
19. BrCanHy	12	/ 66	0.182	10	/ 53	0.189	6	/ 80	0.075
20. FOvSpOp	1	/ 66	0.015	0	/ 54	0.000	2	/ 80	0.025
21. FSpOp	10	/ 65	0.154	7	/ 52	0.135	9	/ 80	0.112
22. FLPalAc	47	/ 62	0.758	40	/ 48	0.833	57	/ 70	0.814
23. TorPal *	0	/ 61	0.000	0	/ 53	0.000	0	/ 79	0.000
24. TorMax	0	/ 67	0.000	0	/ 51	0.000	0	/ 80	0.000
25. FZyFAb	8	/ 66	0.121	7	/ 50	0.140	14	/ 76	0.184
26. FSupOrb	14	/ 67	0.209	9	/ 52	0.173	8	/ 81	0.099
27. FNotFr	11	/ 68	0.162	5	/ 56	0.089	12	/ 81	0.148
28. FAEthEx	18	/ 54	0.333	17	/ 44	0.386	35	/ 77	0.455
29. FPEthAb	1	/ 56	0.018	0	/ 43	0.000	2	/ 77	0.026
30. FlOrbAc	7	/ 60	0.117	2	/ 47	0.043	3	/ 77	0.039

* - Midline trait

APPENDIX 2

TABLE A2.5.5 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

LEFT SIDE ONLY.

	SEDMENT		BADARI		TEITA	
	trait present / no.	freq.	trait present / no.	freq.	trait present / no.	freq.
31. OsInca *	0 / 68	0.000	0 / 57	0.000	2 / 81	0.025
32. SulOrb	13 / 60	0.217	13 / 47	0.277	23 / 74	0.311
33. NasSill	62 / 67	0.925	42 / 51	0.824	31 / 81	0.383
34. FNasal	44 / 55	0.800	35 / 43	0.814	58 / 74	0.784
35. CribOrb	2 / 68	0.029	2 / 56	0.036	4 / 81	0.049
36. SpurTro	3 / 59	0.051	4 / 50	0.080	5 / 81	0.062
37. FosTro	10 / 59	0.169	11 / 50	0.220	25 / 81	0.309
38. GrFront	17 / 68	0.250	15 / 56	0.268	26 / 81	0.321
39. OsSqPar	1 / 66	0.015	1 / 52	0.019	3 / 81	0.037
40. SuJapTr	4 / 59	0.068	5 / 45	0.111	5 / 66	0.076
41. ProcMar	4 / 66	0.061	0 / 50	0.000	4 / 74	0.054
42. FZyTem	45 / 66	0.682	33 / 48	0.688	59 / 78	0.756
43. FZyOrb	59 / 66	0.894	43 / 48	0.896	70 / 79	0.886
44. OsOcMas	2 / 65	0.031	3 / 56	0.054	5 / 80	0.063
45. CanConI	20 / 61	0.328	24 / 52	0.462	28 / 77	0.364
46. TubConP	1 / 59	0.017	2 / 46	0.043	0 / 75	0.000
47. BrJugF	10 / 65	0.154	16 / 53	0.302	5 / 80	0.063
48. TubPhar *	20 / 65	0.308	14 / 52	0.269	10 / 80	0.125
49. FosPhar *	11 / 65	0.169	10 / 53	0.189	5 / 80	0.063
50. FOvOp	2 / 66	0.030	1 / 49	0.020	1 / 80	0.012
51. FVesal	12 / 67	0.179	7 / 45	0.156	8 / 74	0.108
52. BrPtBas	4 / 64	0.063	2 / 48	0.042	1 / 74	0.014
53. BrPtSp	1 / 62	0.016	2 / 43	0.047	0 / 71	0.000
54. BrSpBas	4 / 65	0.062	3 / 51	0.059	3 / 79	0.038
55. SpinFOv	4 / 66	0.061	1 / 49	0.020	2 / 80	0.025
56. FSpAc	3 / 65	0.046	5 / 51	0.098	3 / 79	0.038
57. PerfPt	0 / 53	0.000	2 / 43	0.047	3 / 61	0.049
58. SpurPt	20 / 38	0.526	14 / 23	0.609	20 / 42	0.476
59. BrPal	8 / 65	0.123	11 / 50	0.220	12 / 77	0.156
60. FZyFMu	23 / 58	0.397	17 / 43	0.395	16 / 62	0.258

* - Midline trait

APPENDIX 2

TABLE A2.6.1.

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

RIGHT SIDE ONLY.

	SINDOS			PIERIA			LERNA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	10	/ 30	0.333	5	/ 25	0.200	5	/ 30	0.167
2. OsAtLam *	1	/ 27	0.037	6	/ 25	0.240	1	/ 26	0.038
3. OsLambd	8	/ 29	0.276	14	/ 25	0.560	11	/ 29	0.379
4. FPariet	4	/ 27	0.148	5	/ 25	0.200	5	/ 25	0.200
5. OsBreg *	0	/ 27	0.000	0	/ 25	0.000	0	/ 33	0.000
6. SuMetop *	1	/ 33	0.030	1	/ 26	0.038	3	/ 36	0.083
7. OsCoron	2	/ 25	0.080	1	/ 25	0.040	0	/ 31	0.000
8. OsPter	2	/ 17	0.118	1	/ 23	0.043	0	/ 21	0.000
9. FrTemAr	0	/ 19	0.000	3	/ 23	0.130	0	/ 25	0.000
10. OsPaNot	2	/ 26	0.077	4	/ 25	0.160	2	/ 26	0.077
11. OsAster	2	/ 27	0.074	5	/ 25	0.200	1	/ 26	0.038
12. TorAud	0	/ 29	0.000	0	/ 26	0.000	1	/ 34	0.029
13. FHusch	3	/ 27	0.111	5	/ 26	0.192	5	/ 28	0.179
14. FMasEx	14	/ 24	0.583	8	/ 16	0.500	15	/ 20	0.750
15. FMasAb	6	/ 30	0.200	9	/ 25	0.360	8	/ 28	0.286
16. CanConP	12	/ 20	0.600	13	/ 18	0.722	10	/ 12	0.833
17. BifaCon	2	/ 21	0.095	0	/ 17	0.000	0	/ 10	0.000
18. TubConA	4	/ 23	0.174	3	/ 23	0.130	3	/ 15	0.200
19. BrCanHy	4	/ 22	0.182	8	/ 23	0.348	1	/ 11	0.091
20. FOvSpOp	0	/ 25	0.000	0	/ 20	0.000	1	/ 14	0.071
21. FSpOp	5	/ 23	0.217	10	/ 19	0.526	1	/ 13	0.077
22. FLPalAc	11	/ 17	0.647	15	/ 17	0.882	15	/ 17	0.882
23. TorPal *	2	/ 20	0.100	1	/ 20	0.050	0	/ 19	0.000
24. TorMax	1	/ 25	0.040	0	/ 18	0.000	0	/ 27	0.000
25. FZyFAb	5	/ 20	0.250	5	/ 23	0.217	14	/ 33	0.424
26. FSupOrb	5	/ 24	0.208	5	/ 25	0.200	5	/ 28	0.179
27. FNotFr	3	/ 25	0.120	2	/ 25	0.080	5	/ 32	0.156
28. FAEthEx	5	/ 16	0.313	7	/ 14	0.500	1	/ 5	0.200
29. FPEthAb	0	/ 16	0.000	0	/ 15	0.000	0	/ 6	0.000
30. FIOrbAc	0	/ 17	0.000	3	/ 18	0.167	5	/ 22	0.227

* - Midline trait

APPENDIX 2

TABLE A2.6.1 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

RIGHT SIDE ONLY.

	SINDOS			PIERIA			LERNA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
31. OsInca *	1	/ 29	0.034	1	/ 26	0.038	0	/ 26	0.000
32. SuIOrb	6	/ 18	0.333	10	/ 19	0.526	9	/ 25	0.360
33. NasSill	15	/ 22	0.682	13	/ 18	0.722	22	/ 31	0.710
34. FNasal	13	/ 15	0.867	13	/ 17	0.765	13	/ 19	0.684
35. CribOrb	2	/ 24	0.083	1	/ 24	0.042	3	/ 29	0.103
36. SpurTro	1	/ 21	0.048	4	/ 20	0.200	1	/ 16	0.063
37. FosTro	4	/ 21	0.190	5	/ 20	0.250	2	/ 17	0.118
38. GrFront	7	/ 26	0.269	5	/ 26	0.192	5	/ 32	0.156
39. OsSqPar	1	/ 24	0.042	1	/ 24	0.042	1	/ 27	0.037
40. SuJapTr	0	/ 18	0.000	0	/ 17	0.000	2	/ 25	0.080
41. ProcMar	11	/ 21	0.524	8	/ 23	0.348	8	/ 31	0.258
42. FZyTem	11	/ 20	0.550	19	/ 22	0.864	23	/ 33	0.697
43. FZyOrb	15	/ 22	0.682	17	/ 23	0.739	26	/ 32	0.813
44. OsOcMas	1	/ 27	0.037	4	/ 25	0.160	0	/ 22	0.000
45. CanConI	0	/ 20	0.000	0	/ 16	0.000	1	/ 8	0.125
46. TubConP	1	/ 22	0.045	0	/ 18	0.000	1	/ 17	0.059
47. BrJugF	1	/ 22	0.045	1	/ 23	0.043	0	/ 13	0.000
48. TubPhar *	10	/ 27	0.370	9	/ 21	0.429	4	/ 15	0.267
49. FosPhar *	3	/ 27	0.111	4	/ 21	0.190	1	/ 16	0.063
50. FOvOp	1	/ 21	0.048	0	/ 19	0.000	0	/ 7	0.000
51. FVesal	8	/ 23	0.348	12	/ 19	0.632	6	/ 13	0.462
52. BrPtBas	2	/ 23	0.087	2	/ 19	0.105	0	/ 12	0.000
53. BrPtSp	2	/ 23	0.087	2	/ 16	0.125	1	/ 10	0.100
54. BrSpBas	2	/ 25	0.080	2	/ 20	0.100	0	/ 10	0.000
55. SpinFOv	1	/ 21	0.048	0	/ 21	0.000	0	/ 10	0.000
56. FSpAc	0	/ 22	0.000	1	/ 20	0.050	0	/ 12	0.000
57. PerfPt	0	/ 13	0.000	0	/ 11	0.000	0	/ 7	0.000
58. SpurPt	8	/ 12	0.667	2	/ 12	0.167	2	/ 5	0.400
59. BrPal	1	/ 24	0.042	3	/ 18	0.167	5	/ 19	0.263
60. FZyFMu	7	/ 15	0.467	6	/ 18	0.333	7	/ 19	0.368

* - Midline trait

APPENDIX 2

TABLE A2.6.2 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooledsexes.

RIGHT SIDE ONLY.

	ATHENS-M		ATHENS-G	
	trait present no.	freq.	trait present no.	freq.
1. HiNuLin	12 / 27	0.444	8 / 17	0.471
2. OsAtLam *	3 / 26	0.115	3 / 19	0.158
3. OsLambd	9 / 25	0.360	6 / 19	0.316
4. FPariet	6 / 27	0.222	3 / 18	0.167
5. OsBreg *	0 / 28	0.000	0 / 19	0.000
6. SuMetop *	2 / 28	0.071	1 / 20	0.050
7. OsCoron	0 / 26	0.000	0 / 17	0.000
8. OsPter	0 / 23	0.000	1 / 13	0.077
9. FrTemAr	1 / 24	0.042	0 / 16	0.000
10. OsPaNot	2 / 24	0.083	3 / 15	0.200
11. OsAster	2 / 25	0.080	2 / 20	0.100
12. TorAud	0 / 27	0.000	0 / 20	0.000
13. FHusch	5 / 24	0.208	3 / 19	0.158
14. FMasEx	8 / 20	0.400	5 / 14	0.357
15. FMasAb	6 / 26	0.231	4 / 18	0.222
16. CanConP	13 / 19	0.684	6 / 13	0.462
17. BifaCon	0 / 20	0.000	1 / 15	0.067
18. TubConA	7 / 23	0.304	3 / 15	0.200
19. BrCanHy	8 / 25	0.320	4 / 16	0.250
20. FOvSpOp	0 / 24	0.000	0 / 13	0.000
21. FSpOp	0 / 23	0.000	3 / 10	0.300
22. FLPalAc	11 / 13	0.846	7 / 11	0.636
23. TorPal *	0 / 18	0.000	0 / 16	0.000
24. TorMax	0 / 23	0.000	0 / 14	0.000
25. FZyFAb	4 / 21	0.190	1 / 14	0.071
26. FSupOrb	9 / 27	0.333	4 / 15	0.267
27. FNotFr	3 / 26	0.115	1 / 16	0.063
28. FAEthEx	5 / 10	0.500	1 / 4	0.250
29. FPEthAb	0 / 8	0.000	0 / 4	0.000
30. FIOrbAc	2 / 13	0.154	2 / 9	0.222

* - Midline trait

APPENDIX 2

TABLE A2.6.2 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooledsexes.

RIGHT SIDE ONLY.

	ATHENS-M		ATHENS-G	
	trait present no.	freq.	trait present no.	freq.
31. OsInca *	0 / 28	0.000	0 / 19	0.000
32. SulOrb	6 / 17	0.353	4 / 10	0.400
33. NasSill	15 / 22	0.682	8 / 14	0.571
34. FNasal	8 / 10	0.800	6 / 10	0.600
35. CribOrb	2 / 25	0.080	1 / 17	0.059
36. SpurTro	3 / 17	0.176	2 / 11	0.182
37. FosTro	3 / 18	0.167	1 / 12	0.083
38. GrFront	6 / 28	0.214	1 / 19	0.053
39. OsSqPar	0 / 19	0.000	0 / 13	0.000
40. SuJapTr	1 / 15	0.067	0 / 13	0.000
41. ProcMar	6 / 21	0.286	3 / 14	0.214
42. FZyTem	18 / 21	0.857	11 / 15	0.733
43. FZyOrb	20 / 23	0.870	11 / 14	0.786
44. OsOcMas	1 / 24	0.042	1 / 18	0.056
45. CanConI	2 / 20	0.100	1 / 13	0.077
46. TubConP	0 / 20	0.000	0 / 13	0.000
47. BrJugF	2 / 21	0.095	0 / 12	0.000
48. TubPhar *	6 / 24	0.250	3 / 17	0.176
49. FosPhar *	6 / 24	0.250	2 / 17	0.118
50. FOvOp	1 / 22	0.045	0 / 11	0.000
51. FVesal	5 / 22	0.227	6 / 12	0.500
52. BrPtBas	1 / 22	0.045	1 / 12	0.083
53. BrPtSp	0 / 19	0.000	1 / 10	0.100
54. BrSpBas	2 / 22	0.091	0 / 11	0.000
55. SpinFOv	2 / 20	0.100	1 / 11	0.091
56. FSpAc	0 / 22	0.000	1 / 12	0.083
57. PerfPt	1 / 6	0.167	1 / 9	0.111
58. SpurPt	1 / 5	0.200	3 / 7	0.429
59. BrPal	3 / 22	0.136	1 / 14	0.071
60. FZyFMu	5 / 17	0.294	8 / 13	0.615

* - Midline trait

TABLE A2.6.3.

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooledsexes.

RIGHT SIDE ONLY.

	FORTETSA			PYRGOS		
	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	5	/ 11	0.455	13	/ 18	0.722
2. OsAtLam *	2	/ 11	0.182	0	/ 21	0.000
3. OsLambd	1	/ 11	0.091	5	/ 22	0.227
4. FPariet	6	/ 10	0.600	7	/ 22	0.318
5. OsBreg *	0	/ 11	0.000	0	/ 25	0.000
6. SuMetop *	0	/ 11	0.000	3	/ 24	0.125
7. OsCoron	0	/ 10	0.000	0	/ 20	0.000
8. OsPter	1	/ 7	0.143	0	/ 10	0.000
9. FrTemAr	0	/ 8	0.000	0	/ 11	0.000
10. OsPaNot	0	/ 9	0.000	0	/ 12	0.000
11. OsAster	0	/ 11	0.000	0	/ 14	0.000
12. TorAud	0	/ 9	0.000	0	/ 19	0.000
13. FHusch	2	/ 9	0.222	1	/ 18	0.056
14. FMasEx	6	/ 7	0.857	7	/ 10	0.700
15. FMasAb	3	/ 10	0.300	4	/ 14	0.286
16. CanConP	3	/ 8	0.375	4	/ 5	0.800
17. BifaCon	1	/ 8	0.125	0	/ 8	0.000
18. TubConA	1	/ 7	0.143	2	/ 10	0.200
19. BrCanHy	3	/ 9	0.333	2	/ 9	0.222
20. FOvSpOp	0	/ 8	0.000	0	/ 9	0.000
21. FSpOp	1	/ 8	0.125	3	/ 9	0.333
22. FLPalAc	5	/ 7	0.714	5	/ 5	1.000
23. TorPal *	0	/ 6	0.000	1	/ 5	0.200
24. TorMax	0	/ 7	0.000	0	/ 5	0.000
25. FZyFAb	1	/ 7	0.143	1	/ 10	0.100
26. FSupOrb	4	/ 11	0.364	1	/ 18	0.056
27. FNotFr	1	/ 11	0.091	3	/ 14	0.214
28. FAEthEx	1	/ 6	0.167	0	/ 0	9.999
29. FPEthAb	0	/ 6	0.000	0	/ 0	9.999
30. FlOrbAc	0	/ 7	0.000	1	/ 6	0.167

* - Midline trait

TABLE A2.6.3. (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooledsexes.

RIGHT SIDE ONLY.

	FORTETSA		PYRGOS	
	trait present no.	freq.	trait present no.	freq.
31. OsInca *	0 / 11	0.000	2 / 21	0.095
32. SulOrb	0 / 6	0.000	2 / 4	0.500
33. NasSill	5 / 7	0.714	5 / 6	0.833
34. FNasal	5 / 6	0.833	3 / 4	0.750
35. CribOrb	0 / 9	0.000	3 / 13	0.231
36. SpurTro	0 / 8	0.000	2 / 9	0.222
37. FosTro	2 / 8	0.250	3 / 11	0.273
38. GrFront	1 / 11	0.091	2 / 20	0.100
39. OsSqPar	0 / 8	0.000	0 / 10	0.000
40. SuJapTr	0 / 7	0.000	0 / 9	0.000
41. ProcMar	2 / 7	0.286	4 / 11	0.364
42. FZyTem	4 / 7	0.571	8 / 11	0.727
43. FZyOrb	5 / 7	0.714	9 / 10	0.900
44. OsOcMas	0 / 10	0.000	0 / 13	0.000
45. CanConI	0 / 9	0.000	0 / 8	0.000
46. TubConP	0 / 8	0.000	0 / 8	0.000
47. BrJugF	1 / 9	0.111	1 / 4	0.250
48. TubPhar *	1 / 8	0.125	3 / 9	0.333
49. FosPhar *	3 / 8	0.375	3 / 9	0.333
50. FOvOp	0 / 6	0.000	0 / 8	0.000
51. FVesal	2 / 7	0.286	5 / 11	0.455
52. BrPtBas	0 / 8	0.000	0 / 10	0.000
53. BrPtSp	0 / 8	0.000	0 / 9	0.000
54. BrSpBas	1 / 8	0.125	0 / 10	0.000
55. SpinFOv	0 / 6	0.000	0 / 10	0.000
56. FSpAc	0 / 8	0.000	0 / 10	0.000
57. PerfPt	1 / 3	0.333	0 / 1	0.000
58. SpurPt	1 / 2	0.500	0 / 1	0.000
59. BrPal	1 / 7	0.143	0 / 4	0.000
60. FZyFMu	3 / 5	0.600	3 / 9	0.333

* - Midline trait

APPENDIX 2

TABLE A2.6.4 .

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

RIGHT SIDE ONLY.

	GIZA		KERMA		NAQADA	
	trait present / no.	freq.	trait present / no.	freq.	trait present / no.	freq.
1. HiNuLin	43 / 107	0.402	42 / 84	0.500	61 / 101	0.604
2. OsAtLam *	19 / 106	0.179	5 / 84	0.060	10 / 101	0.099
3. OsLambd	45 / 107	0.421	15 / 84	0.179	33 / 101	0.327
4. FPariet	55 / 107	0.514	49 / 84	0.583	48 / 100	0.480
5. OsBreg *	1 / 107	0.009	1 / 84	0.012	2 / 100	0.020
6. SuMetop *	1 / 107	0.009	2 / 84	0.024	2 / 100	0.020
7. OsCoron	3 / 107	0.028	0 / 84	0.000	4 / 100	0.040
8. OsPter	11 / 107	0.103	10 / 81	0.123	15 / 101	0.149
9. FrTemAr	0 / 107	0.000	6 / 81	0.074	1 / 101	0.010
10. OsPaNot	8 / 107	0.075	7 / 84	0.083	9 / 101	0.089
11. OsAster	4 / 107	0.037	5 / 84	0.060	6 / 101	0.059
12. TorAud	1 / 107	0.009	1 / 84	0.012	2 / 101	0.020
13. FHusch	20 / 106	0.189	17 / 83	0.205	13 / 100	0.130
14. FMasEx	35 / 61	0.574	26 / 42	0.619	26 / 66	0.394
15. FMasAb	46 / 107	0.430	42 / 84	0.500	35 / 101	0.347
16. CanConP	66 / 107	0.617	48 / 76	0.632	69 / 101	0.683
17. BifaCon	0 / 107	0.000	0 / 78	0.000	0 / 99	0.000
18. TubConA	13 / 107	0.121	7 / 83	0.084	14 / 101	0.139
19. BrCanHy	24 / 107	0.224	7 / 82	0.085	17 / 101	0.168
20. FOvSpOp	1 / 107	0.009	0 / 83	0.000	3 / 101	0.030
21. FSpOp	16 / 107	0.150	10 / 83	0.120	12 / 100	0.120
22. FLPalAc	98 / 107	0.916	67 / 82	0.817	84 / 99	0.848
23. TorPal *	0 / 107	0.000	0 / 82	0.000	0 / 100	0.000
24. TorMax	0 / 107	0.000	0 / 82	0.000	0 / 99	0.000
25. FZyFAb	21 / 107	0.196	17 / 83	0.205	16 / 101	0.158
26. FSupOrb	18 / 107	0.168	11 / 84	0.131	17 / 100	0.170
27. FNotFr	9 / 107	0.084	14 / 84	0.167	8 / 101	0.079
28. FAEthEx	34 / 103	0.330	28 / 78	0.359	35 / 90	0.389
29. FPEthAb	2 / 103	0.019	2 / 76	0.026	5 / 93	0.054
30. FIOrbAc	9 / 107	0.084	2 / 82	0.024	5 / 100	0.050

* - Midline trait

TABLE A2.6.4 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

RIGHT SIDE ONLY.

	GIZA		KERMA		NAQADA	
	trait present / no.	freq.	trait present / no.	freq.	trait present / no.	freq.
31. OsInca *	3 / 107	0.028	3 / 84	0.036	2 / 101	0.020
32. SulOrb	37 / 107	0.346	13 / 82	0.159	38 / 99	0.384
33. NasSill	87 / 107	0.813	50 / 83	0.602	85 / 99	0.859
34. FNasal	87 / 102	0.853	56 / 64	0.875	73 / 81	0.901
35. CribOrb	15 / 107	0.140	6 / 84	0.071	4 / 101	0.040
36. SpurTro	14 / 107	0.131	12 / 83	0.145	13 / 96	0.135
37. FosTro	23 / 107	0.215	19 / 83	0.229	32 / 96	0.333
38. GrFront	23 / 107	0.215	21 / 84	0.250	33 / 101	0.327
39. OsSqPar	3 / 107	0.028	2 / 82	0.024	6 / 101	0.059
40. SuJapTr	11 / 107	0.103	1 / 83	0.012	5 / 93	0.054
41. ProcMar	3 / 107	0.028	9 / 83	0.108	4 / 100	0.040
42. FZyTem	73 / 107	0.682	61 / 83	0.735	73 / 101	0.723
43. FZyOrb	94 / 107	0.879	67 / 83	0.807	96 / 101	0.950
44. OsOcMas	1 / 106	0.009	5 / 82	0.061	3 / 101	0.030
45. CanConI	66 / 107	0.617	29 / 80	0.363	56 / 101	0.554
46. TubConP	1 / 107	0.009	0 / 78	0.000	0 / 97	0.000
47. BrJugF	19 / 107	0.178	19 / 82	0.232	21 / 101	0.208
48. TubPhar *	33 / 107	0.308	30 / 84	0.357	30 / 100	0.300
49. FosPhar *	19 / 107	0.178	20 / 84	0.238	19 / 100	0.190
50. FOvOp	3 / 107	0.028	0 / 84	0.000	2 / 99	0.020
51. FVesal	20 / 107	0.187	17 / 84	0.202	16 / 99	0.162
52. BrPtBas	6 / 107	0.056	5 / 84	0.060	4 / 100	0.040
53. BrPtSp	2 / 105	0.019	3 / 84	0.036	1 / 96	0.010
54. BrSpBas	11 / 107	0.103	7 / 82	0.085	3 / 101	0.030
55. SpinFOv	8 / 107	0.075	11 / 83	0.133	1 / 101	0.010
56. FSpAc	3 / 107	0.028	0 / 83	0.000	4 / 101	0.040
57. PerfPt	6 / 103	0.058	3 / 70	0.043	4 / 79	0.051
58. SpurPt	56 / 100	0.560	30 / 63	0.476	34 / 61	0.557
59. BrPal	17 / 107	0.159	18 / 82	0.220	20 / 100	0.200
60. FZyFMu	34 / 86	0.395	36 / 66	0.545	33 / 85	0.388

* - Midline trait

APPENDIX 2

TABLE A2.6.5.

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

RIGHT SIDE ONLY.

	SEDMENT			BADARI			TEITA		
	trait present	no.	freq.	trait present	no.	freq.	trait present	no.	freq.
1. HiNuLin	41	/ 68	0.603	31	/ 56	0.554	35	/ 81	0.432
2. OsAtLam *	10	/ 68	0.147	6	/ 57	0.105	12	/ 81	0.148
3. OsLambd	22	/ 68	0.324	21	/ 56	0.375	32	/ 81	0.395
4. FPariet	28	/ 68	0.412	20	/ 57	0.351	44	/ 81	0.543
5. OsBreg *	0	/ 68	0.000	0	/ 57	0.000	0	/ 81	0.000
6. SuMetop *	3	/ 67	0.045	4	/ 56	0.071	1	/ 80	0.012
7. OsCoron	2	/ 68	0.029	2	/ 55	0.036	0	/ 81	0.000
8. OsPter	13	/ 68	0.191	14	/ 50	0.280	6	/ 79	0.076
9. FrTemAr	1	/ 68	0.015	3	/ 50	0.060	4	/ 80	0.050
10. OsPaNot	7	/ 68	0.103	7	/ 54	0.130	13	/ 81	0.160
11. OsAster	8	/ 68	0.118	3	/ 55	0.055	4	/ 81	0.049
12. TorAud	5	/ 68	0.074	2	/ 56	0.036	0	/ 81	0.000
13. FHusch	10	/ 67	0.149	8	/ 57	0.140	29	/ 81	0.358
14. FMasEx	14	/ 40	0.350	19	/ 38	0.500	18	/ 48	0.375
15. FMasAb	28	/ 68	0.412	17	/ 55	0.309	32	/ 80	0.400
16. CanConP	30	/ 64	0.469	29	/ 50	0.580	41	/ 80	0.513
17. BifaCon	0	/ 62	0.000	1	/ 49	0.020	0	/ 62	0.000
18. TubConA	11	/ 66	0.167	5	/ 49	0.102	2	/ 77	0.026
19. BrCanHy	9	/ 66	0.136	10	/ 54	0.185	8	/ 81	0.099
20. FOvSpOp	1	/ 67	0.015	1	/ 51	0.020	2	/ 80	0.025
21. FSpOp	17	/ 67	0.254	10	/ 51	0.196	11	/ 80	0.137
22. FLPalAc	50	/ 62	0.806	37	/ 49	0.755	52	/ 67	0.776
23. TorPal *	0	/ 61	0.000	0	/ 53	0.000	0	/ 79	0.000
24. TorMax	0	/ 65	0.000	0	/ 51	0.000	0	/ 81	0.000
25. FZyFAb	7	/ 65	0.108	11	/ 51	0.216	17	/ 78	0.218
26. FSupOrb	14	/ 68	0.206	13	/ 54	0.241	7	/ 81	0.086
27. FNotFr	8	/ 68	0.118	4	/ 56	0.071	11	/ 80	0.137
28. FAEthEx	21	/ 57	0.368	11	/ 38	0.289	34	/ 73	0.466
29. FPEthAb	0	/ 56	0.000	1	/ 43	0.023	1	/ 78	0.013
30. FlOrbAc	7	/ 63	0.111	2	/ 48	0.042	4	/ 78	0.051

* - Midline trait

TABLE A2.6.5 (CONTINUED).

NON-METRIC TRAITS: RAW FREQUENCIES.

13 Greek and African groups - pooled sexes.

RIGHT SIDE ONLY.

	SEDMENT		BADARI		TEITA	
	trait present / no.	freq.	trait present / no.	freq.	trait present / no.	freq.
31. OsInca *	0 / 68	0.000	0 / 57	0.000	2 / 81	0.025
32. SulOrb	19 / 64	0.297	17 / 48	0.354	25 / 76	0.329
33. NasSill	59 / 66	0.894	41 / 54	0.759	24 / 79	0.304
34. FNasal	48 / 52	0.923	40 / 42	0.952	62 / 73	0.849
35. CribOrb	1 / 68	0.015	3 / 55	0.055	3 / 81	0.037
36. SpurTro	4 / 63	0.063	5 / 51	0.098	11 / 79	0.139
37. FosTro	6 / 63	0.095	14 / 51	0.275	28 / 80	0.350
38. GrFront	25 / 68	0.368	17 / 54	0.315	27 / 81	0.333
39. OsSqPar	4 / 67	0.060	3 / 49	0.061	4 / 81	0.049
40. SuJapTr	5 / 59	0.085	4 / 46	0.087	5 / 67	0.075
41. ProcMar	4 / 64	0.063	0 / 49	0.000	4 / 76	0.053
42. FZyTem	47 / 65	0.723	37 / 51	0.725	62 / 80	0.775
43. FZyOrb	62 / 65	0.954	48 / 51	0.941	61 / 80	0.763
44. OsOcMas	4 / 68	0.059	4 / 53	0.075	11 / 81	0.136
45. CanConI	29 / 64	0.453	22 / 49	0.449	26 / 78	0.333
46. TubConP	0 / 57	0.000	1 / 47	0.021	0 / 75	0.000
47. BrJugF	10 / 66	0.152	13 / 48	0.271	6 / 81	0.074
48. TubPhar *	20 / 65	0.308	14 / 52	0.269	10 / 80	0.125
49. FosPhar *	11 / 65	0.169	10 / 53	0.189	5 / 80	0.063
50. FOvOp	4 / 66	0.061	1 / 49	0.020	0 / 81	0.000
51. FVesal	13 / 66	0.197	10 / 46	0.217	13 / 78	0.167
52. BrPtBas	0 / 66	0.000	2 / 49	0.041	3 / 78	0.038
53. BrPtSp	1 / 63	0.016	0 / 42	0.000	0 / 72	0.000
54. BrSpBas	5 / 67	0.075	1 / 53	0.019	2 / 80	0.025
55. SpinFOv	1 / 67	0.015	1 / 46	0.022	2 / 81	0.025
56. FSpAc	5 / 67	0.075	4 / 48	0.083	4 / 80	0.050
57. PerfPt	3 / 57	0.053	3 / 36	0.083	2 / 63	0.032
58. SpurPt	21 / 42	0.500	15 / 19	0.789	26 / 48	0.542
59. BrPal	8 / 65	0.123	15 / 53	0.283	19 / 79	0.241
60. FZyFMu	28 / 58	0.483	13 / 40	0.325	21 / 61	0.344

* - Midline trait

APPENDIX 3

GENERALISED LINEAR MODELS.

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APPENDIX 3

GENERALISED LINEAR MODELS.

A3.1. Defining statistical models.

The analysis of numerical data presents problems for the human mind which cannot encompass the large number of values present in the raw data. Generalised linear models (GLMs), like multivariate analysis, replace the original voluminous data with a summary describing their general characteristics in terms of a limited number of quantities. Models may be regarded as theories which generate patterns of numbers which can, in some sense, replace the data. They assume that the data under investigation have a definite structure which will explain the values obtained and predict future values.

Each data value is considered as a random variable **Y**, the *dependent* or *y-variable*. A model attempts to express the y-variable in terms of other more fundamental variables, the *components* of the data structure. Some of the components will have fixed values; these are called *systematic components*.. From the sum of all the systematic components, E(Y), the expected value or *mean* of the y-variate can be derived. The expected value, E(Y) is termed μ. This value is the fitted value, or value predicted by the model. The model also contains a *random component*, which accounts for the discrepancy between the observed value y and its expected value μ.

A3.2. Contingency tables - log-linear models

Contingency table data is analysed using *log-linear* models. In these models, the fitted value μ is related to the sum of the systematic components by a logarithmic relationship. The formula for this type of model is as follows,

$$\log_e(\mu) = \sum_{i=1}^{p} (\beta_i x_i).$$

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($\beta_i x_i$) are the systematic components, where x_i are the *explanatory variables* and βi the parameters associated with these variables. The sum of the systematic components is termed the *linear predictor*, denoted by η, such that

$$\eta = \sum_{i=1}^{p} (\beta_i x_i).$$

$\text{Log}_e(\mu)$ gives the fitted or predicted value for a cell of the table. This is related to y, the actual or *observed* value by the following formula,

$$y_j = \mu_j + \varepsilon_j$$

For any one cell, the random component ε denotes the discrepancy between the expected value and the value actually observed. This random variation might obscure systematic patterns of variation in the data. However, if a large number (J) of cells is considered using the same model, the random variation may be described statistically, and so summarised in terms of its mass behaviour.

A3.3. Building models using GLIM.

In chapter 5 (section 5.3.1.2.1) the procedure for building models for contingency table data has been described, but a brief recap follows. Table A3.1 may be referred to as an example of such data. Each model is a collection of *terms*, where a term represents either a *factor* (margin of the table) such as sex or population, or an interaction of factors. Hence a model postulating that the pattern of counts in table A3.1 is affected only by sex (x), population (p) and an interaction of these two factors (p.x) is represented by the following collection of terms:

$$\text{model} = p + x + p.x. \qquad \text{(a3.1)}$$

The GLIM program, given such a set of terms, will generate a mathematical formula with the appropriate explanatory variables, derive the associated ß parameters (maximum likelihood estimates) and produce a goodness-of-fit statistic for assessing how adequately the model reproduces the original data.

To understand the output from a GLIM modelling session, the relationship between the model above (as given to the program) and the model's mathematical formula must be

examined. Each term in the model introduces a number of explanatory variables into the formula. These variables are 'dummy variables' having values of 0 or 1, depending on which cell of the table is being considered. The number of dummy variables associated with each term is dependant on the number of categories or *levels* of the factor. Hence the sex factor in formula a3.1 gives rise to two explanatory variables, $x_{X(M)}$ for the male level and $x_{X(F)}$ for the female, and for any cell, one of these variables will take the value 1 and the other 0. Similarly, the population factor gives rise to $x_{P(G)}$ and $x_{P(T)}$ for Giza and Teita respectively. Note that factor levels are exclusive; any cell can appear in only one of the levels. For interaction terms, the number of variables is the product of the number of levels in each factor.

Since the explanatory variables are dummy variables, the word 'parameter' is often used to refer to the component βx as well as to β itself. The model given above (a3.1) would generate a formula for the linear predictor including the following parameters,

$$\begin{aligned} & & [\ \text{sex parameters}\ ] & & [\ \text{population parameters}\ ] \\ \eta \quad = \quad K \ + \ & \beta_{X(M)}x_{X(M)} \ + \ \beta_{X(F)}x_{X(F)} \ + \ \beta_{P(G)}x_{P(G)} \ + \ \beta_{P(T)}x_{P(T)} & & \\ & + \ \beta_{I(MG)}x_{I(MG)} \ + \ \beta_{I(MT)}x_{I(MT)} & & [\text{interaction parameters}] \\ & + \ \beta_{I(FG)}x_{I(FG)} \ + \ \beta_{I(FT)}x_{I(FT)}, & & \end{aligned} \qquad \text{(a3.2)}$$

where K is a constant, and the subscripts X, P and I refer to parameters derived from the sex, population and interaction terms respectively.

A3.4. Glim example programs

Three examples illustrating the use of the GLIM package (Baker and Nelder 1978, Rothamstead Experimental Station) now follow.

Example 1.

This is based on the data in table a3.1, showing the distribution of the midline trait *pharyngeal tubercle* in males and females from two populations, Giza and Teita.

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The parameters displayed by GLIM are relative rather than absolute parameter values. The factor levels are referenced by numbers (1 to N where N is the number of levels in that factor) and the parameter values for level 1 of each factor are set to zero. The cell(s) corresponding to level 1 for all of the factors (in this case, males from Giza who show absence of the trait) is taken as a reference cell.

The linear predictor for the fitted value of the reference cell is denoted by %gm (the grand mean). This is equivalent to the constant K in (a3.2), since all parameters for the reference cell are set to 0. The exponent of this value gives the fitted value for cell 1 (the reference cell). For cells corresponding to factor levels other than zero, the printed estimates are added to the grand mean to give the linear predictor for that cell.

In this example, the models employed, and the sequence in which they are fitted, do not represent good modelling practice. Example 1 is meant to illustrate the action of the different factors in the model, and parameter estimates and fitted values are therefore printed at every stage. The printed output (in lower-case letters) is annotated with upper-case letters in square brackets to facilitate understanding of what is, at first sight, dauntingly complex output.

Example 2

This is based on the data in table a3.2 and shows the analysis of the bilateral trait 'parietal foramen' in 6 groups. It illustrates the modelling procedure adopted for most of the traits examined in this work.

Example 3

This is the analysis of the data in table a3.3 and shows the analysis of the bilateral trait 'Epigenetic bone present' in 6 groups, as undertaken in this work. This trait illustrates the method of modelling when three-factor interactions are present.

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TABLE A3.1

PHARYNGEAL TUBERCLE IN MALES AND FEMALES

FROM TWO POPULATIONS (GIZA AND TEITA).

		Trait absent	Trait present	Totals
GIZA	Males	34	21	55
	Females	40	12	52
	Total	74	33	107
KENYA	Males	25	8	33
	Females	47	2	49
	Total	72	10	82
COMBINED	Males	59	29	88
	Females	87	14	101
GRAND TOTAL		146	43	189

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GLIM EXAMPLE PROGRAM 1.

```
GLIM 3.12 (c)1977 Royal Statistical Society, London

$units 8 $data ct $dinput 7$                    [ READ 'ct', 8 UNITS OF DATA,
                                                          FROM FILE 7 ]

$fac p 2 x 2 t 2                                [ DECLARE THE FACTORS :
                                                        'p'  (POPULATION),
$calc p = %gl(2,1)                                      'x'  (SEX),
     : x = %gl(2,4)                                     't'  (TRAIT EXPRESSION),
     : t = %gl(2,2)                                     EACH OF 2 LEVELS, AND MATCH
                                                        FACTOR LEVELS TO THE DATA ]

$yvar ct  $err p $                              [ DECLARE Y-VARIABLE (DATA)
                                                  "CT", AND ERROR DISTRIBUTION
                                                  (FOR CONTINGENCY TABLES THIS
                                                  IS THE POISSON DISTRIBUTION)]

$look ct$                                       [ LIST DATA "CT" ]

                                                [ 'p'    ' x'    't'
1        34.00                                    1       1       1
2        25.00                                    2       1       1
3        21.00                                    1       1       2      FACTOR
4         8.00                                    2       1       2      LEVELS
5        40.00                                    1       2       1      FOR
6        47.00                                    2       2       1      EACH
7        12.00                                    1       2       2      DATA
8         2.00                                    2       2       2      VALUE.]

$fit$                                           [ FIT THE NULL MODEL ]
        scaled
cycle   deviance      df
 4        85.96       7                         [ "RESIDUAL DEVIANCE" OF THE
                                                   NULL MODEL - THIS VALUE IS
                                                          HIGHLY SIGNIFICANT ]

$dis ur                                         [ PRINT PARAMETER ESTIMATES,
                                                          FITTED VALUES, RESIDUALS ]

        estimate        s.e.          parameter
1       3.162           0.7273E-01      %gm                   [ EXPONENT(3.162)= 23.62
scale parameter taken as 1.000                                  -DISCREPANCY DUE TO
                                                                ROUNDING ERRORS ]

unit    observed        fitted          residual
1       34              23.63           2.135                 [ RESIDUALS ARE
2       25              23.63           .2829                   LOG-LIKELIHOOD
3       21              23.63           -.5401                DEVIANCES OF THE
4       8               23.63           -3.215                FITTED VALUES.
5       40              23.63           3.369                 THE EIGHT VALUES
6       47              23.63           4.809                 SUM TO ZERO. ]
7       12              23.63           -2.392
8       2               23.63           -4.449
```

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```
$fit p $
          scaled
cycle    deviance        df
 4         82.64          6

$dis ur
          estimate        s.e.        parameter
1          3.287        0.9667E-01      %gm
2          -.2661          .1467         p(2)
scale parameter taken as 1.000
```

[MODEL 1 - FIT FACTOR 'p']

[HIGHLY SIGNIFICANT]

[EXP(3.287)
= 26.76
EXP(3.287-.2661)
= 20.51]

[p(1) IS THE REFERENCE LEVEL
AND ITS PARAMETER VALUE = 0.
THE NEGATIVE VALUE OF p(2)
INDICATES THAT GROUP 2 IS
SMALLER THAN GROUP 1]

unit	observed	fitted	residual
1	34	26.75	1.402
2	25	20.50	.9939
3	21	26.75	-1.112
4	8	20.50	-2.761
5	40	26.75	2.562
6	47	20.50	5.853
7	12	26.75	-2.852
8	2	20.50	-4.086

['p': PARAMETERS
1 %gm + 0
2 %gm +.2661
1 %gm + 0
2 %gm +.2661
AND SO ON]

[THESE FITTED VALUES CAN
BE DERIVED FROM THE
MARGINAL TOTALS :
e.g. GP. 1 = $\frac{\text{107 SKULLS}}{\text{4 CELLS}}$ = 26.75]

```
$fit x $
          scaled
cycle    deviance        df
 4         85.07          6

$dis ur
          estimate        s.e.        parameter
1          3.091          .1066          %gm
2          .1378          .1458          x(2)
scale parameter taken as 1.000
```

[MODEL 2 - FIT FACTOR 'x']

[EXP(3.091)
= 22.0
EXP(3.091 +.1378)
= 25.25]

[x(2) IS POSITIVE : THERE ARE
MORE FEMALES THAN MALES]

unit	observed	fitted	residual
1	34	22.00	2.558
2	25	22.00	.6396
3	21	22.00	-.2132
4	8	22.00	-2.985
5	40	25.25	2.935
6	47	25.25	4.328
7	12	25.25	-2.637
8	2	25.25	-4.627

['x': PARAMETERS
1 %gm + 0
1 "
1 "
1 "
2 %gm +.1378
2 "
2 "
2 "
]

[THESE FITTED VALUES CAN
BE DERIVED FROM THE
MARGINAL TOTALS :
e.g. 88 MALES / 4 CELLS = 22]

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```
$fit t $                                                    [ MODEL 3 - FIT FACTOR 't' ]
            scaled
cycle    deviance        df
 4         26.65          6

$dis ur
            estimate          s.e.          parameter       [ EXP(3.597)
1            3.597          0.8276E-01        %gm                          = 36.49
2           -1.222          .1735             t(2)          EXP(3.597 -1.222)
scale parameter taken as 1.000                                             = 10.75  ]
                                                            [ THE NEGATIVE VALUE OF t(2)
                                                              SHOWS THAT TRAIT PRESENCE
                                                                IS SIGNIFICANTLY LESS
                                                                COMMON THAN ABSENCE.]
unit     observed        fitted          residual
1          34            36.50           -.4138                [ SIMILARLY,
2          25            36.50           -1.903                 THESE FITTED
3          21            10.75            3.126                 VALUES CAN BE
4           8            10.75           -.8387                 DERIVED FROM
5          40            36.50            .5793                 THE MARGINAL
6          47            36.50            1.738                      TOTALS. ]
7          12            10.75            .3812
8           2            10.75           -2.669

$fit +p $                                                   [ MODEL 4 - ADD FACTOR 'p'
            scaled                                            TO THE PREVIOUS MODEL.
cycle    deviance        df                                       NEW MODEL = p + x ]
 4         81.75          5

$dis ur
            estimate          s.e.          parameter       [ EXP(3.215)
1            3.215          .1242             %gm                          = 24.90
2            .1378          .1458             x(2)          EXP(3.215 +.1378)
3           -.2661          .1467             p(2)                         = 28.58
scale parameter taken as 1.000                              EXP(3.215 -.2661)
                                                                           = 19.08
                                                            EXP(3.215 +.1378 -.2661)
                                                                           = 21.90 ]

unit     observed        fitted          residual                [ 'p'    'x'
1          34            24.91            1.821                   1       1
2          25            19.09            1.353                   2       1
3          21            24.91           -.7834                   1       1
4           8            19.09           -2.538                   2       1
5          40            28.59            2.134                   1       2
6          47            21.91            5.360                   2       2
7          12            28.59           -3.103                   1       2
8           2            21.91           -4.254                   2       2 ]

                                                            [ THESE FITTED VALUES CAN BE
                                                            DERIVED FROM THE MARGINAL
                                                            TOTALS USING THIS FORMULA:

                                                                GROUP TOTAL * SEX TOTAL
                                                                GRAND TOTAL * 2 CELLS  ]
```

APPENDIX 3

$fit +t $ [MODEL 5 - ADD FACTOR 't'
NEW MODEL = p + x + t]

cycle	scaled deviance	df
4	22.44	4

$dis ur [N.B. THE FACTOR
PARAMETER VALUES
ARE IDENTICAL IN
MODELS 1 TO 6
BUT %gm VARIES
IN EACH MODEL]

	estimate	s.e.	parameter
1	3.650	.1303	%gm
2	.1378	.1458	x(2)
3	-.2661	.1468	p(2)
4	-1.222	.1735	t(2)

scale parameter taken as 1.000

unit	observed	fitted	residual	['p'	'x'	't']
1	34	38.49	-.7230	1	1	1
2	25	29.49	-.8274	2	1	1
3	21	11.33	2.871	1	1	2
4	8	8.686	-.2329	2	1	2
5	40	44.17	-.6275	1	2	1
6	47	33.85	2.260	2	2	1
7	12	13.01	-.2798	1	2	2
8	2	9.970	-2.524	2	2	2]

[THESE FITTED VALUES CAN
BE DERIVED FROM THE
MARGINAL TOTALS USING
THIS FORMULA :

$$\frac{\text{SEX TOTAL} * \text{GROUP TOTAL} * \text{EXPRESSION TOTAL}}{\text{GRAND TOTAL} * \text{GRAND TOTAL}}$$]

$fit p +x +p.x $ [MODEL 6 = p + x + p.x
THIS IS THE MINIMUM MODEL
REQUIRED BY THE FIXED
MARGINAL TOTALS.]

cycle	scaled deviance	df
5	79.42	4

$dis ur [N.B. THE FACTOR
PARAMETER VALUES
HAVE NOW CHANGED.
WHEN THE TERM 'p.x'
IS INCLUDED THE
FACTORS CEASE TO
BE INDEPENDENT.]

	estimate	s.e.	parameter
1	3.314	.1348	%gm
2	-.5108	.2202	p(2)
3	-0.5609E-01	.1934	x(2)
4	.4514	.2969	p(2).x(2)

scale parameter taken as 1.000

unit	observed	fitted	residual
1	34	27.50	1.240
2	25	16.50	2.093
3	21	27.50	-1.240
4	8	16.50	-2.093
5	40	26.00	2.746
6	47	24.50	4.546
7	12	26.00	-2.746
8	2	24.50	-4.546

[THE PARAMETER
p(2).x(2) IS USED IN
THE CALCULATION
OF UNIT 8 ONLY.
PARAMETERS p(1).x(2)
AND p(2).x(1) HAVE
THE VALUE 0]

[THE FITTED VALUES ARE HALF
THE NUMBER OF EACH SEX
IN EACH GROUP. IT IS
THEREFORE APPARENT THAT
THIS MINIMUM MODEL
CONTAINS NO INFORMATION
OF BIOLOGICAL VALUE.]

APPENDIX 3

$fit p +x +t +p.x $

[MODEL 7 - p + x + t + p.x
THE MINIMUM MODEL USED
IN THE PRESENT STUDY.]

cycle	scaled deviance	df
4	20.11	3

$dis ur

	estimate	s.e.	parameter
1	3.749	.1405	%gm
2	-.5108	.2202	p(2)
3	-0.5609E-01	.1934	x(2)
4	-1.222	.1735	t(2)
5	.4514	.2968	p(2).x(2)

scale parameter taken as 1.000

unit	observed	fitted	residual
1	34	42.49	-1.302
2	25	25.49	-0.9746E-01
3	21	12.51	2.399
4	8	7.508	.1796
5	40	40.17	-0.2671E-01
6	47	37.85	1.487
7	12	11.83	0.4922E-01
8	2	11.15	-2.740

$fit +x.t +p.t $

[MODEL 8 - THE MAXIMAL MODEL
p + x + t + p.x + p.t + x.t]

cycle	scaled deviance	df
3	2.142	1

[DEVIANCE INSIGNIFICANT]

$dis ur

	estimate	s.e.	parameter
1	3.474	.1720	%gm
2	-.1889	.2481	p(2)
3	.2567	.2248	x(2)
4	-.3510	.2584	t(2)
5	.2707	.3087	p(2).x(2)
6	-1.097	.4044	p(2).t(2)
7	-1.050	.3739	x(2).t(2)

scale parameter taken as 1.000

[THE PARAMETER
VALUES FOR p.t
AND x.t ARE
SIGNIFICANT, BUT
THE t-VALUES ARE
ONLY APPROXIMATE
AND MODELS WHICH
EXCLUDE THESE
TERMS SHOULD BE
TESTED BEFORE
CONCLUDING THAT
SEX AND GROUP
ASSOCIATIONS ARE
SIGNIFICANT.]

unit	observed	fitted	residual
1	34	32.28	.3031
2	25	26.72	-.3332
3	21	22.72	-.3613
4	8	6.278	.6874
5	40	41.72	-.2666
6	47	45.28	.2559
7	12	10.28	.5372
8	2	3.722	-.8927

APPENDIX 3

$fit -p.t$ [MODEL 9 - MAXIMAL - p.t]

cycle	scaled deviance	df
4	10.26	2

[DIFFERENCE = 8.478 FOR 1 df - p.t HIGHLY SIGNIFICANT]

$dis ur

	estimate	s.e.	parameter
1	3.608	.1542	%gm
2	-.5108	.2202	p(2)
3	.1945	.2112	x(2)
4	-.7102	.2268	t(2)
5	.4514	.2969	p(2).x(2)
6	-1.117	.3665	x(2).t(2)

scale parameter taken as 1.000

unit	observed	fitted	residual
1	34	36.88	-.4734
2	25	22.13	.6112
3	21	18.13	.6753
4	8	10.88	-.8718
5	40	44.79	-.7160
6	47	42.21	.7376
7	12	7.208	1.785
8	2	6.792	-1.839

$fit +p.t -x.t$ [MODEL 10 - MAXIMAL - x.t]

cycle	scaled deviance	df
4	10.43	2

[DIFFERENCE = 8.288 FOR 1 df - x.t HIGHLY SIGNIFICANT]

$dis ur

	estimate	s.e.	parameter
1	3.639	.1495	%gm
2	-.2721	.2331	p(2)
3	-0.5609E-01	.1934	x(2)
4	-.8076	.2093	t(2)
5	.4514	.2968	p(2).x(2)
6	-1.167	.3970	p(2).t(2)

scale parameter taken as 1.000

unit	observed	fitted	residual
1	34	38.04	-.6546
2	25	28.98	-.7386
3	21	16.96	.9803
4	8	4.024	1.982
5	40	35.96	.6732
6	47	43.02	.6061
7	12	16.04	-1.008
8	2	5.976	-1.626

APPENDIX 3

$fit +x.t +p.x.t$ [MODEL 11 - THE FULL MODEL (FOR INTEREST ONLY)]

cycle	scaled deviance	df
3	0.1064E-13	0

$dis ur

	estimate	s.e.	parameter
1	3.526	.1715	%gm
2	-.3075	.2635	p(2)
3	.1625	.2333	x(2)
4	-.4818	.2775	t(2)
5	.4688	.3401	p(2).x(2)
6	-.6576	.4920	p(2).t(2)
7	-.7221	.4305	x(2).t(2)
8	-1.295	.9335	p(2).x(2).t(2)

scale parameter taken as 1.000

unit	observed	fitted	residual
1	34	34.00	0.0000E+00
2	25	25.00	0.0000E+00
3	21	21.00	0.0000E+00
4	8	8.000	0.0000E+00
5	40	40.00	0.0000E+00
6	47	47.00	0.0000E+00
7	12	12.00	0.0000E+00
8	2	2.000	-0.2107E-07

$stop

APPENDIX 3

TABLE A3.2

PARIETAL FORAMEN IN MALES AND FEMALES

FROM SIX AFRICAN POPULATIONS.

Group	Sex	Trait expression (both sides) L-R-	L+R-	L-R+	L+R+	Sex Total	Group Total
GIZA	Male	18	5	14	18	55	107
	Female	21	8	12	11	52	
KERMA	Male	18	5	13	16	52	111
	Female	16	9	16	18	59	
NAQADA	Male	18	9	11	11	49	100
	Female	14	11	8	18	51	
SEDMENT	Male	16	6	10	7	39	68
	Female	14	4	5	6	29	
BADARI	Male	10	12	7	7	36	57
	Female	12	3	2	4	21	
TEITA	Male	14	3	7	10	34	83
	Female	17	4	14	14	49	
TOTALS FOR ALL GROUPS	Male	94	40	62	69	265	
	Female	94	39	57	71	261	
	Both	188	79	119	140	526	526

The Kerma group contains 29 additional skulls (from those in which the first thirty traits were examined to compare with A.C. Berry's scoring criteria).
Similarly, the Teita sample includes the two extra female crania whose traits were scored, but whose measurements could not be located in the Duckworth Museum's record of Howells' data files; these two were excluded from the distance measures.

APPENDIX 3

GLIM EXAMPLE PROGRAM 2.

```
GLIM 3.12 (c)1977 Royal Statistical Society, London

$units 48 $data ct $dinput 7$

$fac  p6  x2  l2  r2$

$calc p=%gl(6,1) : x=%gl(2,24) : l=%gl(2,6) : r=%gl(2,12)  $

$yvar ct  $err p  $fit  $
            scaled
cycle    deviance          df
  4        118.1           47


$fit p + x + l + r + p.x $                    [(1) FIT THE MINIMUM MODEL .....]
            scaled
cycle    deviance          df                 [....A VERY POOR FIT TO THE DATA ]
  4        65.74           34                                (p < 0.001)


$fit + p.l + p.r + x.l + x.r + l.r $          [(2) ADD REMAINING 2-FACTOR TERMS]
            scaled
cycle    deviance          df                 [.... DEVIANCE NOT SIGNIFICANT
  3        16.09           21                                - AN ADEQUATE FIT ]


                                              [EACH OF THE TWO-FACTOR TERMS
                                                IS NOW TESTED FOR SIGNIFICANCE ]


$fit  - l.r  $                                [(3) DROP THE TERM 'l.r' AND
            scaled                                    COMPARE DEVIANCE WITH (2) ]
cycle    deviance          df
  4        50.13           22                 [DIFFERENCE = 16.1 for 1 df (p < 0.001) ]


$fit  + l.r - p.l $                           [(4) REPLACE 'l.r', DROP 'p.l'
            scaled                                    AND COMPARE WITH (2) ]
cycle    deviance          df
  3        22.70           26                 [DIFFERENCE = 6.6 for 5df (ns)]


$fit  + p.l - p.r $                           [(5) REPLACE 'p.l', DROP 'p.r'
            scaled                                    AND COMPARE WITH (2) ]
cycle    deviance          df
  3        27.60           26                 [DIFFERENCE = 11.5 for 5df (p < 0.05)]


$fit  + p.r - x.1 $                           [(6) REPLACE 'p.r', DROP 'x.l'
            scaled                                    AND COMPARE WITH (2) ]
cycle    deviance          df
  3        16.23           22                 [DIFFERENCE = 0.14 for 1df (ns)]
```

```
$fit + x.l - x.r $                                  [(7) REPLACE 'x.l', DROP 'x.r'
                                                          AND COMPARE WITH (2) ]
          scaled
cycle   deviance        df
  3       16.38         22                          [DIFFERENCE = 0.29 for 1df (ns)]


$fit - x.l - p.l $                                  [(8) REMOVE NON-SIGNIFICANT
                                                          2-FACTOR TERMS]
          scaled
cycle   deviance        df                          [.... DEVIANCE NOT SIGNIFICANT
  3       22.98         28                                - AN ADEQUATE FIT ]


$dis l

linear predictor                                    [DISPLAY TERMS IN
%gm  p  x  l  r  p.x  p.r  l.r                            CURRENT MODEL (8) ]


$dis  usr                                           [DISPLAY THE FOLLOWING...]


                                                    [....THE VALUES AND STANDARD
                                                          ERRORS OF THE PARAMETERS]

          estimate          s.e.          parameter
 1          2.935          .1721          %gm
 2          .1728          .2431          p(2)
 3       0.4785E-01        .2402          p(3)
 4          .1528          .2530          p(4)
 5          .1343          .2552          p(5)
 6          .5406          .2678          p(6)
 7       0.5609E-01        .1934          x(2)
 8          .8670          .1340          l(2)          [ DIFFERENCE BETWEEN 'l' AND 'r'
 9          .3708          .2086          r(2)                = 0.4962 ,
10          .1824          .2713          p(2).x(2)     ST. ERROR OF THIS DIFFERENCE
11       0.9610E-01        .2782          p(3).x(2)           (SEE NEXT PAGE )
12          .2402          .3123          p(4).x(2)           = 0.2255.
13          .4829          .3356          p(5).x(2)     THE FREQUENCY OF TRAIT
14          .4215          .2953          p(6).x(2)     PRESENCE ON THE LEFT SIDE
15          .2158          .2722          p(2).r(2)       IS SIGNIFICANTLY (p < 0.05)
16          .1361          .2783          p(3).r(2)     HIGHER THAN THAT
17          .4128          .3132          p(4).r(2)                 ON THE RIGHT. ]
18          .6713          .3381          p(5).r(2)
19          .1130          .2931          p(6).r(2)
20          1.030          .1830          l(2).r(2)

scale parameter taken as        1.000
```

[....STANDARD ERRORS OF THE DIFFERENCES BETWEEN THE PARAMETERS]

s.e. of differences

1	0.0000E+00									
2	.3806	0.0000E+00								
3	.3788	.2463	0.0000E+00							
4	.3870	.2588	.2561	0.0000E+00						
5	.3885	.2610	.2583	.2702	0.0000E+00					
6	.3968	.2733	.2707	.2821	.2841	0.0000E+00				
7	.3216	.2453	.2424	.2550	.2573	.2698	0.0000E+00			
8	.2413	.2776	.2750	.2863	.2883	.2995	.2353	0.0000E+00		
9	.3388	.2533	.2505	.2628	.2650	.2771	.2845	.2255	0.0000E+00	
10	.2586	.4555	.4094	.4171	.4184	.4262	.4311	.3026	.3422	0.0000E+00
11	.2659	.4158	.4607	.4216	.4230	.4307	.4355	.3088	.3477	.2760
12	.3013	.4393	.4377	.4991	.4461	.4534	.4580	.3398	.3756	.3103
13	.3255	.4562	.4546	.4615	.5191	.4698	.4742	.3614	.3952	.3338
14	.2837	.4274	.4258	.4331	.4344	.5041	.4466	.3243	.3616	.2932
15	.2555	.4619	.4126	.4202	.4215	.4293	.3339	.3034	.4387	.3843
16	.2620	.4184	.4605	.4241	.4255	.4332	.3389	.3089	.4425	.3886
17	.2988	.4424	.4407	.5006	.4491	.4564	.3681	.3407	.4652	.4144
18	.3248	.4603	.4587	.4655	.5212	.4738	.3895	.3637	.4823	.4334
19	.2777	.4284	.4267	.4340	.4353	.4987	.3512	.3223	.4520	.3994
20	.2291	.3043	.3020	.3122	.3141	.3244	.2663	.2956	.3232	.3272
	1	2	3	4	5	6	7	8	9	10

[THE STANDARD ERROR OF THE DIFFERENCE BETWEEN PARAMETERS 8 AND 9 ('I' AND 'r') = 0.2255]

11	0.0000E+00									
12	.3164	0.0000E+00								
13	.3395	.3679	0.0000E+00							
14	.2997	.3315	.3536	0.0000E+00						
15	.3892	.4143	.4322	.4017	0.0000E+00					
16	.3935	.4183	.4360	.4058	.2770	.0000E+00				
17	.4189	.4423	.4591	.4305	.3121	.3174	0.0000E+00			
18	.4378	.4602	.4764	.4489	.3370	.3419	.3709	0.0000E+00		
19	.4041	.4283	.4456	.4161	.2919	.2976	.3305	.3541	0.0000E+00	
20	.3330	.3620	.3823	.3474	.3280	.3331	.3628	.3844	.3456	0.0000E+00
	11	12	13	14	15	16	17	18	19	20

scale parameter taken as 1.000

APPENDIX 3

[...FITTED VALUES AND RESIDUALS
FOR EACH CELL OF THE TABLE]

unit	observed	fitted	residual
1	18	18.82	-.1891
2	18	15.83	.5446
3	18	17.94	0.1394E-01
4	16	16.15	-0.3815E-01
5	10	16.45	-1.591
6	14	10.96	.9181
7	5	7.909	-1.034
8	5	6.653	-.6410
9	9	7.539	.5321
10	6	6.788	-.3024
11	12	6.914	1.934
12	3	4.606	-.7482
13	14	12.99	.2804
14	13	13.56	-.1521
15	11	10.81	0.5887E-01
16	10	7.378	.9651
17	7	5.804	.4966
18	7	8.470	-.5050
19	18	15.28	.6954
20	16	15.95	0.1170E-01
21	11	12.71	-.4806
22	7	8.680	-.5704
23	7	6.828	0.6586E-01
24	10	9.964	0.1135E-01
25	21	17.79	.7601
26	16	17.96	-.4635
27	14	18.67	-1.081
28	14	12.01	.5738
29	12	9.598	.7752
30	17	15.80	.3029
31	8	7.477	.1912
32	9	7.549	.5281
33	11	7.847	1.126
34	4	5.047	-.4662
35	3	4.033	-.5145
36	4	6.638	-1.024
37	12	12.28	-0.8015E-01
38	16	15.39	.1566
39	8	11.25	-.9683
40	5	5.486	-.2077
41	2	3.385	-.7530
42	14	12.21	.5135
43	11	14.45	-.9071
44	18	18.10	-0.2369E-01
45	18	13.23	1.311
46	6	6.455	-.1790
47	4	3.983	0.8561E-02
48	14	14.36	-0.9504E-01

$stop

APPENDIX 3

TABLE A3.3

EPIPTERIC BONE IN MALES AND FEMALES

FROM SIX AFRICAN POPULATIONS.

Group	Sex	Trait expression (both sides) L-R-	L+R-	L-R+	L+R+	Sex Total	Group Total
GIZA	Male	46	4	3	2	55	107
	Female	45	1	4	2	52	
KERMA	Male	45	2	3	0	50	107
	Female	39	4	4	10	57	
NAQADA	Male	41	1	1	5	48	99
	Female	38	4	3	6	51	
SEDMENT	Male	33	1	3	1	38	67
	Female	19	2	1	7	29	
BADARI	Male	16	2	9	3	30	48
	Female	13	3	0	2	18	
TEITA	Male	33	0	0	0	33	79
	Female	39	1	3	3	46	
TOTALS FOR ALL GROUPS	Male	214	10	19	11	254	
	Female	193	15	15	30	253	
	Both	407	25	34	41	507	507

The Kerma group contains 25 additional skulls (from those in which the first thirty traits were examined to compare with A.C. Berry's scoring criteria). Similarly, the Teita sample includes the two extra female crania whose traits were scored, but whose measurements could not be located in the Duckworth Museum's record of Howells' data files; these two were excluded from the distance measures.

APPENDIX 3

GLIM EXAMPLE PROGRAM 3.

```
GLIM 3.12 (c)1977 Royal Statistical Society, London

$units 48 $data ct $dinput 7  $

$fac  p 6   x 2  l 2  r 2  $

$calc p=%gl(6,1) : x=%gl(2,24) : l=%gl(2,6) : r=%gl(2,12)  $

$yvar ct   $err p   $fit  $
                scaled
cycle     deviance          df
  5         803.7           47


$fit p + x + l + r + p.x $                    [(1) FIT THE MINIMUM MODEL .....]
                scaled
cycle     deviance          df                [....A VERY POOR FIT TO THE DATA]
  5         171.7           34                          (p < 0.001)


$fit + p.l + p.r + x.l + x.r + l.r $          [(2) ADD REMAINING 2-FACTOR TERMS]
                scaled
cycle     deviance          df                [... STILL AN INADEQUATE FIT]
  4         43.18           21                          (p<0.01)


$fit + p.x.l + p.x.r + p.l.r + x.l.r $        [(3) ADD ALL THE 3 FACTOR TERMS....]
                scaled
cycle     deviance          df                [.... DEVIANCE NOT SIGNIFICANT
 10         7.487            5                          - AN ADEQUATE FIT ]

                                              [EACH OF THE THREE-FACTOR TERMS
                                               IS NOW TESTED FOR SIGNIFICANCE ]


$fit - p.x.l $                                [(4) DROP THE TERM 'p.x.l' AND
                scaled                              COMPARE DEVIANCE WITH (3) ]
cycle     deviance          df
  9         16.74           10                [DIFFERENCE = 9.25 for 5 df (ns) ]


$fit + p.x.l - p.x.r $                        [(5) REPLACE 'p.x.l', DROP 'p.x.r'
                scaled                              AND COMPARE WITH (3) ]
cycle     deviance          df
  9         21.29           10                [DIFFERENCE = 13.8 for 5df (p<0.02)]


$fit + p.x.r - p.l.r $                        [(6) REPLACE 'p.x.r', DROP 'p.l.r'
                scaled                              AND COMPARE WITH (3) ]
cycle     deviance          df
 10         10.73           10                [DIFFERENCE = 3.24 for 5 df (ns) ]
```

APPENDIX 3

```
$fit + p.l.r - x.l.r $
          scaled
cycle    deviance        df
 10       8.771           6
```

[(7) REPLACE 'p.x.r', DROP 'p.l.r'
AND COMPARE WITH (3)]

[DIFFERENCE = 1.28 for 1 df (ns)]

```
$fit - p.l.r - p.x.l $

          scaled
cycle    deviance        df
 8        24.34          16
```

[(8) REMOVE NON-SIGNIFICANT
3-FACTOR TERMS]

[.... DEVIANCE NOT SIGNIFICANT
- AN ADEQUATE FIT]

```
$dis l

linear predictor
%gm  p  x  l  r  p.x  p.l  x.l  p.r  x.r  l.r  p.x.r
```

[DISPLAY TERMS IN
CURRENT MODEL (8)]

[NOW TEST THOSE 2-FACTOR TERMS
WHICH ARE NOT CONTAINED
IN THE TERM 'p.x.r']

```
$fit - p.l $
          scaled
cycle    deviance        df
 8        31.05          21
```

[(9) DROP THE TERM 'p.l' AND
COMPARE DEVIANCE WITH (8)]

[DIFFERENCE = 6.7 for 5df (ns)]

```
$fit + p.l - x.l $
          scaled
cycle    deviance        df
 8        32.82          17
```

[(10) REPLACE 'p.l', DROP 'x.l'
AND COMPARE WITH (8)]

[DIFFERENCE = 8.5 for 1df (p < 0.01)]

```
$fit + x.l - l.r $
          scaled
cycle    deviance        df
 9        111.3          17
```

[(11) REPLACE 'x.l', DROP 'l.r'
AND COMPARE WITH (8)]

[DIFFERENCE = 87 for 1df (p < 0.001)]

```
$fit + l.r - p.l $

          scaled
cycle    deviance        df
 8        31.05          21
```

[(12) REMOVE NON-SIGNIFICANT
2-FACTOR TERMS .....]

[.... DEVIANCE NOT SIGNIFICANT
- AN ADEQUATE FIT]

APPENDIX 3

```
$dis lusr                                          [DISPLAY THE FOLLOWING.....

                                                   [..... TERMS IN THE
                                                         CURRENT MODEL (12) ]

linear predictor
%gm  p  x  l  r  p.x  x.l  p.r  x.r  l.r  p.x.r

                                                   [....THE VALUES AND STANDARD
                                                         ERRORS OF THE PARAMETERS]
```

	estimate	s.e.	parameter
1	3.874	.1418	%gm
2	-0.6188E-01	.2032	p(2)
3	-.1744	.2093	p(3)
4	-.3857	.2223	p(4)
5	-1.022	.2749	p(5)
6	-.4155	.2243	p(6)
7	-.1297	.2052	x(2)
8	-3.263	.2971	l(2)
9	-2.818	.4853	r(2)
10	-0.5566E-02	.2937	p(2).x(2)
11	0.8338E-01	.2989	p(3).x(2)
12	-.3985	.3446	p(4).x(2)
13	-0.3440E-01	.3997	p(5).x(2)
14	.2758	.3115	p(6).x(2)
15	.8270	.3234	x(2).l(2)
16	-.4490	.7580	p(2).r(2)
17	.3567	.6407	p(3).r(2)
18	.1625	.7067	p(4).r(2)
19	1.897	.5991	p(5).r(2)
20	-9.183	32.94	p(6).r(2)
21	-.1239	.6577	x(2).r(2)
22	2.959	.3153	l(2).r(2)
23	1.364	.9261	p(2).x(2).r(2)
24	.1398	.8566	p(3).x(2).r(2)
25	.9093	.9276	p(4).x(2).r(2)
26	-1.940	1.053	p(5).x(2).r(2)
27	9.323	32.94	p(6).x(2).r(2)

scale parameter taken as 1.000

APPENDIX 3

s.e. of differences [....STANDARD ERRORS OF THE DIFFERENCES BETWEEN THE PARAMETERS]

1	0.0000E+00									
2	.3184	0.0000E+00								
3	.3224	.2123	0.0000E+00							
4	.3310	.2251	.2307	0.0000E+00						
5	.3683	.2772	.2817	.2915	0.0000E+00					
6	.3323	.2271	.2326	.2444	.2930	0.0000E+00				
7	.3199	.2083	.2143	.2270	.2787	.2289	0.0000E+00			
8	.3390	.3599	.3634	.3711	.4048	.3723	.3564	0.0000E+00		
9	.5428	.4866	.4892	.4949	.5206	.4958	.4901	.5931	0.0000E+00	
10	.2577	.4584	.4124	.4191	.4493	.4202	.4603	.4178	.6015	0.0000E+00
11	.2636	.4131	.4699	.4228	.4527	.4239	.4636	.4215	.6040	.3036
12	.3145	.4473	.4501	.5167	.4841	.4572	.4943	.4550	.6279	.3487
13	.3741	.4910	.4936	.4992	.6217	.5001	.5342	.4981	.6598	.4032
14	.2778	.4223	.4253	.4318	.4611	.4979	.4718	.4305	.6104	.3160
15	.3458	.3819	.3852	.3924	.4244	.3935	.3968	.5751	.5411	.4369
16	.7448	.8357	.8114	.8149	.8308	.8154	.8104	.8142	1.118	.7605
17	.6250	.7013	.7361	.7070	.7253	.7077	.7018	.7062	1.042	.6758
18	.6925	.7620	.7637	.8048	.7842	.7679	.7626	.7666	1.084	.7387
19	.5822	.6634	.6654	.6696	.7652	.6702	.6641	.6687	1.017	.6365
20	32.94	32.94	32.94	32.94	32.94	32.94	32.94	32.94	32.95	32.94
21	.6443	.7168	.7186	.7225	.7404	.7231	.7439	.6739	1.058	.6598
22	.3406	.3751	.3784	.3857	.4183	.3869	.3722	.5320	.6183	.4309
23	.9580	.9036	.9282	.9312	.9451	.9317	.9035	.9726	.8082	1.057
24	.8910	.8574	.8307	.8621	.8771	.8626	.8321	.9067	.7275	.9506
25	.9595	.9283	.9296	.9006	.9466	.9331	.9050	.9740	.8099	1.015
26	1.082	1.054	1.055	1.058	1.017	1.058	1.034	1.095	.9515	1.131
27	32.94	32.94	32.94	32.94	32.94	32.94	32.94	32.94	32.94	32.95
	1	2	3	4	5	6	7	8	9	10

11	0.0000E+00									
12	.3531	0.0000E+00								
13	.4070	.4417	0.0000E+00							
14	.3208	.3638	.4164	0.0000E+00						
15	.4404	.4726	.5142	.4490	0.0000E+00					
16	.7899	.8083	.8333	.7948	.8241	0.0000E+00				
17	.6420	.6995	.7282	.6838	.7177	.7383	0.0000E+00			
18	.7408	.7207	.7869	.7460	.7772	.7963	.6855	0.0000E+00		
19	.6389	.6616	.6063	.6449	.6808	.7025	.5739	.6468	0.0000E+00	
20	32.94	32.94	32.94	32.94	32.94	32.94	32.94	32.94	32.94	0.0000E+00
21	.6622	.6840	.7134	.6679	.7954	.7531	.6349	.7014	.5929	32.94
22	.4344	.4671	.5091	.4432	.4351	.8210	.7140	.7738	.6770	32.94
23	1.015	1.030	1.049	1.019	.9810	1.607	1.307	1.341	1.287	32.96
24	1.001	.9675	.9885	.9562	.9156	1.322	1.402	1.294	1.238	32.96
25	1.017	1.103	1.051	1.020	.9823	1.369	1.308	1.536	1.288	32.96
26	1.133	1.145	1.261	1.136	1.102	1.458	1.400	1.432	1.479	32.96
27	32.95	32.95	32.95	32.95	32.94	32.96	32.96	32.96	32.96	65.88
	11	12	13	14	15	16	17	18	19	20

21	0.0000E+00						
22	.7518	0.0000E+00					
23	1.452	.9783	0.0000E+00				
24	1.408	.9128	.8802	0.0000E+00			
25	1.453	.9797	.9494	.8817	0.0000E+00		
26	1.536	1.100	1.073	1.013	1.074	0.0000E+00	
27	32.96	32.94	32.94	32.94	32.94	32.95	0.0000E+00
	21	22	23	24	25	26	27

scale parameter taken as 1.000

APPENDIX 3

[...FITTED VALUES AND RESIDUALS
FOR EACH CELL OF THE TABLE]

unit	observed	fitted	residual
1	46	48.16	-.3108
2	45	45.27	-0.3970E-01
3	41	40.45	0.8625E-01
4	33	32.75	0.4431E-01
5	16	17.34	-.3210
6	33	31.78	.2158
7	4	1.843	1.588
8	2	1.733	.2029
9	1	1.549	-.4408
10	1	1.254	-.2265
11	2	.6637	1.640
12	0	1.217	-1.103
13	3	2.876	0.7283E-01
14	3	1.726	.9698
15	1	3.452	-1.320
16	3	2.301	.4607
17	9	6.904	.7979
18	0	0.1951E-03	-0.1397E-01
19	2	2.124	-0.8476E-01
20	0	1.274	-1.129
21	5	2.548	1.536
22	1	1.699	-.5362
23	3	5.096	-.9286
24	0	0.1440E-03	-0.1200E-01
25	45	42.30	.4155
26	39	39.54	-0.8573E-01
27	38	38.62	-0.9970E-01
28	19	19.31	-0.7050E-01
29	13	14.71	-.4464
30	39	36.78	.3660
31	1	3.702	-1.404
32	4	3.461	.2898
33	4	3.380	.3370
34	2	1.690	.2383
35	3	1.288	1.509
36	1	3.219	-1.237
37	4	2.232	1.183
38	4	5.208	-.5295
39	3	3.348	-.1903
40	1	2.976	-1.146
41	0	.7440	-.8626
42	3	2.232	.5139
43	2	3.768	-.9107
44	10	8.792	.4075
45	6	5.652	.1465
46	7	5.024	.8817
47	2	1.256	.6639
48	3	3.768	-.3956

$stop

APPENDIX 4

COMPUTER PACKAGES AND PROGRAMS.

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APPENDIX 4

COMPUTER PACKAGES AND PROGRAMS

A4.1. Index of packages used.

BMDP — BIOMEDICAL PROGRAMS.

BMDP Statistical Software
1964 Westwood Blvd., Suite 202
Los Angeles, CA 90025.
U.S.A.

GENSTAT — A GENERAL STATISTICAL PROGRAM
(Rothamsted Experimental Station)

The Numerical Algorithms Group Limited.
7 Banbury Road
Oxford. OX2 6NN.

GINO-F — GRAPHICAL INPUT/OUTPUT - FORTRAN VERSION

CADCentre Ltd
High Cross
Madingley Road
Cambridge. CB3 0HB

GLIM — GENERALISED LINEAR INTERACTIVE MODELLING

The Numerical Algorithms Group Limited.
7 Banbury Road
Oxford. OX2 6NN.

MDS(X) — THE MDS(X) SERIES OF MULIDIMENSIONAL SCALING PROGRAMS
(University of Edinburgh Program Library Unit.)

The Program Library Unit
18 Buccleuch Place
Edinburgh. EH8 9LN.

MINITAB — General Purpose Statistical Computing System

Minitab Inc.
3081 Enterprise Drive
State College, PA 16801
U.S.A.

APPENDIX 4

A4.2. Program for calculating D^2 values.

(Written in GENSTAT by Dr. S.P. Evans and J. E. Powell)

```
'REFE/NID=900,NUNN=300'D2PROG

'CAPT'          "
          PROGRAM WHICH CALCULATES MAHALANOBIS DISTANCES BETWEEN
        GROUPS WHEN MISSING VALUES ARE PRESENT.  THE VARIANCE-
        COVARIANCE MATRIX  IS DERIVED ONLY FROM COMPLETE DATA-SETS.
        THE MEANS ARE  ESTIMATED USING ALL AVAILABLE DATA.  A PLOT OF
        THE POINTS IS PRODUCED USING PRINCIPLE COMPONENTS ANALYSIS.
                "

'SCAL' NS=257      " NS = NUMBER OF SKULLS "
   :       NG=6       " NG = NUMBER OF GROUPS "
   :       NV=5       " NV = NUMBER OF VARIABLES "

          "
DECLARE FACTOR, GRP
(GROUP NAMES AND NUMBER OF SKULLS IN EACH GROUP )
MALES ONLY FROM 6 AFRICAN SITES
          "

'UNIT' SKULL$NS
'NAME'NAMG=GIZA,KERMA,NAQADA,SEDMENT,BADARI,KENYA
'FACT'GRP$NAMG=55(1),43(2),50(3),39(4),36(5),34(6)
          "
DECLARE SET OF MEASUREMENTS, VSET
          "

'SET'  VSET=GOL,XCB,NPH,OBH,NLB
'VARI'VSET$NS

          "
READ IN THE DATA, USING THE FORMAT STATEMENT BELOW
          "

'INPUT'2
'READ/P'VSET$F,8X,3,9X,3,20X,2,2X,2,5X,2,2/
'INPUT'1

          "
CALCULATE AND PRINT SSP MATRIX AND ASSOCIATED GROUP MEANS
          "

'SET'MEANS=GRPMEANS(1...NV),GRPSIZES
'VARI'MEANS $NG
'DSSP'WSSP$VSET;GRP;MEANS
'SSP/PRIN=SC'WSSP
'PRIN/P'MEANS $ 9.3
'RUN'
'DEVA' VSET
```

APPENDIX 4

```
            "
 REDECLARE STRUCTURES AND READ IN RAW DATA AGAIN
            "

'SET'   VARS=GOL,XCB,NPH,OBH,NLB
'VARI' VARS $NS
'INPUT/REWI=Y'2
'READ/P'VARS$F,8X,3,9X,3,20X,2,2X,2,5X,2,2/
'INPUT'1
'SYMMAT' DMAT,TDMAT$NAMG
'SCAL' NEDMAT,NEWSSP1
'CALC' NEDMAT=NG*(NG-1)*0.5+NG
      :     NEWSSP1=NV*(NV+1)*0.5+NV
'SYMMAT'WSSPMAT,INVMAT $NV
'VARI' POPMNS(1...NG),GRPTOTS(1...NG),MVAL(1...NG),DIFS,DUM $NV
'SCAL' DFWSSP
'RUN'

          "
REMOVE EXTRA ROW FROM SSP MATRIX AND INVERT
          "

'SCAL' S(1...NEDMAT),T(1...NEDMAT),M(1...NEDMAT),LAB(1...4)
'EQUA' WSSPMAT = WSSP
    :          DFWSSP=WSSP $NEWSSP1!(X),1
'CALC' DFWSSP = DFWSSP-NG
'PRINT' DFWSSP
'CALC' INVMAT=INV(WSSPMAT)

          "
CALCULATE THE "BEST ESTIMATE" OF THE MEANS USING ALL AVAILABLE DATA
          "

     'FOR'II=1...NG ; PM=POPMNS(1...NG); MT=MVAL(1...NG); GT=GRPTOTS(1...NG)
     'REST' VARS $GRP=II
        'FOR' SS=S(1...NV) ; TT=T(1...NV) ;  MM=M(1...NV) ; VV=VARS
        'CALC' SS = MEAN(VV)
           :     TT = NVAL(VV)
           :    MM = NMV(VV)
        'REPE'
     'EQUA' PM=S(1...NV)
        :     GT=T(1...NV)
        :    MT=M(1...NV)
     'REST' VARS
     'REPE'
'PRINT/P'POPMNS(1...NG) $ 10.4
'PRIN/P'GRPTOTS(1...NG) $ 10.0
'PRINT/P' MVAL(1...NG) $ 10.0
'RUN'
'CALC'GRPTOTS(1...NG)=GRPTOTS(1...NG)-MVAL(1...NG)
'PRIN/P'GRPTOTS(1...NG) $ 10.0
'RUN'
'DEVA', GRPTOTS(1...NG),MVAL(1...NG)
```

APPENDIX 4

```
"
CALCULATE MAHALANOBIS DISTANCES
"
'SCAL'   I=0 : J=0 : IND=1
'LABEL' LAB(1)
'CALC'   I=I+1
'JUMP'    LAB(4)*(I.GT.NG)
'CALC'   J=0
'LABEL' LAB(2)
'CALC'   J=J+1
'JUMP'    LAB(1)*(J.GT.I)
'ASSIGN' K=S(1...NEDMAT) $IND
'CALC'   IND=IND+1
'JUMP'    LAB(3)*(J.LT.I)
'CALC'   K=0
'GOTO'   LAB(2)
'LABEL' LAB(3)
'ASSIGN' XX = POPMNS(1...NG) $I
'ASSIGN' YY = POPMNS(1...NG) $J
'CALC'   DIFS = XX-YY
'CALC'   DUM =PDT(INVMAT;DIFS)
    :        K =TPDT(DIFS;DUM)
'GOTO'   LAB(2)
'LABEL'  LAB(4)
'EQUA'   DMAT=S(1...NEDMAT)
'CALC'   DMAT = DMAT*DFWSSP
'PRINT'  DMAT $8.4
'CALC'   TDMAT=-0.5*DMAT
    :        DMAT=SQRT(DMAT)
"
PRINT OUT THE MATRIX OF D-VALUES IN A SEPARATE FILE:
"
'OUTPUT' 2
'PRINT'   DMAT $8.4
'OUTPUT' 1
'PRINT'   DMAT $8.4
'PRINT'   TDMAT $8.4
'RUN'

"
PRINT OUT PLOTS OF THE MAHALANOBIS DISTANCES USING PCO:
LABEL THE POINTS AS DECLARED IN "SITE" BELOW
"
'MATRIX' CMPTS $NG,3
'DIAG'   RTS $3
'SCAL'   TRCE
'VARI'   X,Y,Z $ NG
'NAME'  SITE = GZ,KR,NQ,SD,BD,KY
'FACT'   GRPLABELS$ SITE =1...NG
'PCO/PRIN=LTRCD'   TDMAT;CMPTS,RTS,TRCE
'EQUA'   X,Y,Z = CMPTS $(1,2X)NG,X
'GRAPH/EQXY=Y,NCF=101,NRF=61'   X;Y$;GRPLABELS
          :                                  Y;Z$;GRPLABELS
          :                                  X;Z$;GRPLABELS
'RUN'
'CLOSE'
'STOP'
```